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L10: Entry 2 of 11

File: PGPB

Jun 17, 2004.

DOCUMENT-IDENTIFIER: US 20040115767 A1

TITLE: Immunogenic cell surface proteins of helicobacter pylori

Detail Description Paragraph:

[0073] Cell binding factor 2 (HP0175) has a similarity to cell-binding factor 2 of C jejuni (antigen [PEB4A](#)) and is a homologue to Escherichia coli survival protein surA. Here two were identified, but a further two-three isoforms with lower pI's could be proposed with the same M.sub.rs. Cross reactivity with serum from a C. jejuni infected patient was not observed.

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☐ 1. 5874300. 13 Mar 95; 23 Feb 99. *Campylobacter jejuni* antigens and methods for their production and use. Blaser, Martin J., et al. 435/325; 435/252.3 435/252.31 435/252.33 435/254.2 435/254.21 435/320.1 435/348 435/362 435/365 435/367 435/69.3 536/23.7. C12N015/31 C12N015/63 C12N015/70 C12N015/79.

☐ 2. 5470958. 16 Sep 94; 28 Nov 95. Antisera against a PEB1 antigen from *Campylobacter jejuni*. Blaser, Martin J., et al. 530/389.5; 424/164.1 435/252.1 435/7.32 435/822. A61K035/16 A61K039/106.

☐ 3. 5200344. 13 Nov 90; 06 Apr 93. Diagnostic testing for *Campylobacter jejuni* or *Campylobacter coli* infections using novel antigens. Blaser, Martin J., et al. 435/7.32; 435/29 435/7.92 435/961 435/967 436/547 530/389.5. G01N033/569.

Genes Dev. 1996 Dec 15;10(24):3170-82.

[Related Articles, Links](#)

SurA, a periplasmic protein with peptidyl-prolyl isomerase activity, participates in the assembly of outer membrane porins.

Rouviere PE, Gross CA.

Department of Stomatology, University of California, San Francisco 94143-0512, USA.

Little is known about either the process of periplasmic protein folding or how information concerning the folding state in this compartment is communicated. We present evidence that SurA, a periplasmic protein with peptidyl-prolyl isomerase activity, is involved in the maturation and assembly of LamB. LamB is a trimeric outer membrane porin for maltodextrins as well as the bacteriophage lambda receptor in *Escherichia coli*. We demonstrate that SurA is involved in the conversion of unfolded monomers into a newly identified intermediate in LamB assembly, which behaves as a folded monomer. The absence of SurA blocks the assembly pathway and leads to accumulation of species prior to the folded monomer. These species also accumulate when the stress sigma factor sigmaE is induced by LamB overexpression. We suggest that accumulation of species prior to the generation of folded monomer is a stress signal sensed by sigmaE.

PMID: 8985185 [PubMed - indexed for MEDLINE]

Mol Microbiol. 1996 Aug;21(4):871-84.

Related Articles, Links

New components of protein folding in extracytoplasmic compartments of *Escherichia coli* SurA, FkpA and Skp/OmpH.

Missiakas D, Betton JM, Raina S.

Centre Medical Universitaire, Departement de Biochimie Medicale, Geneve, Switzerland.

A global search for extracytoplasmic folding catalysts in *Escherichia coli* was undertaken using different genetic systems that produce unstable or misfolded proteins in the periplasm. The extent of misfolding was monitored by the increased activity of the sigma E regulon that is specifically induced by misfolded proteins in the periplasm. Using multicopy libraries, we cloned two genes, *surA* and *fkpA*, that decreased the sigma E-dependent response constitutively induced by misfolded proteins. According to their sequences and their biochemical activities, SurA and FkpA belong to two different peptidyl prolyl isomerase (PPI) families. Interestingly, *surA* was also selected as a multicopy suppressor of a defined *htrM* (*rfaD*) null mutation. Such mutants produce a defective lipopolysaccharide that is unable to protect outer membrane proteins from degradation during folding. The SurA multicopy suppression effect in *htrM* (*rfaD*) mutant bacteria was directly associated with its ability to catalyse the folding of outer membrane proteins immediately after export. Finally, Tn10 insertions were isolated, which led to an increased activity of the sigma E regulon. Such insertions were mapped to the *dsb* genes encoding catalysts of the protein disulphide isomerase (PDI) family, as well as to the *surA*, *fkpA* and *ompH/skp* genes. We propose that these three proteins (SurA, FkpA and OmpH/Skp) play an active role either as folding catalysts or as chaperones in extracytoplasmic compartments.

PMID: 8878048 [PubMed - indexed for MEDLINE]

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UniProtKB/Swiss-Prot entry P56112

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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information


Entry name	Y175_HELPY
Primary accession number	P56112
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 35, November 1997
Sequence was last modified in	Release 35, November 1997
Annotations were last modified in	Release 47, May 2005
Name and origin of the protein	
Protein name	Hypothetical protein HP0175 [Precursor]
Synonyms	None
Gene name	OrderedLocusNames: HP0175
From	Helicobacter pylori (Campylobacter pylori) [TaxID: 210]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.

References

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=26695 / ATCC 700392;

DOI=10.1038/41483; PubMed=9252185 [NCBI, ExPASy, EBI, Israel, Japan]

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G., , Venter J.C.;
 "The complete genome sequence of the gastric pathogen Helicobacter pylori.";
 Nature 388:539-547(1997).

Comments

- **SIMILARITY:** Belongs to the ppiC/parvulin rotamase family.

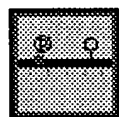
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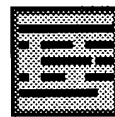
Cross-references

EMBL	AE000538; AAD07245.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	G64541; G64541.	
HSSP	P39159; 1JNS. [HSSP ENTRY / PDB]	
TIGR	HP0175; -. IPR000297; Rotamase.	

InterPro	Graphical view of domain structure.
Pfam	PF00639; Rotamase; 1. Pfam graphical view of domain structure.
PROSITE	PS01096; PPIC_PPIASE_1; 1. PS50198; PPIC_PPIASE_2; 1. PROSITE graphical view of domain structure (profiles).
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOGENOM	[Family / Alignment / Tree]
BLOCKS	P56112.
ProtoNet	P56112.
ProtoMap	P56112.
PRESAGE	P56112.
DIP	P56112.
ModBase	P56112.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords**Complete proteome; Hypothetical protein; Isomerase; Rotamase; Signal.****Features**

Feature table viewer



Feature aligner

Key	From	To	Length	Description
SIGNAL	1	21	21	Potential.
CHAIN	22	299	278	Hypothetical protein HP0175.
DOMAIN	154	253	100	Pp1C.

Sequence information

Length: **299 AA** [This is the length of the unprocessed precursor]
 Molecular weight: **34031 Da** [This is the MW of the unprocessed precursor]

CRC64: **E65F3F2F94B11F5A** [This is a checksum on the sequence]

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MKKNILNLAL VGALSTSFLM AKPAHNANNA THNTKKTDS SAGVLATVDG RPITKSDFDM

      70           80           90          100          110          120
IKQRNPNFDF DKLKEKEKEA LIDQAIRTAL VENEAKTEKL DSTPEFKAMM EAVKKQALVE

     130          140          150          160          170          180
FWAKKQAEV  KKVQIPEKEM QDFYNANKDQ LFKVQEAHAR HILVKTEDEA KRIISEIDKQ

     190          200          210          220          230          240
PKAKKEAKFI ELANRDTIDP NSKNAQNGGD LGKFQKNQMA PDFSKAAFAL TPGDYTKTPV

     250          260          270          280          290
KTEFGYHIIY LISKDSPVTY TYEQAKPTIK GMLQEKLFQE RMNQRIEELR KHAKIVINK

```

P56112 in FASTA
format

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BLAST

BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-
MODEL



NPSA Sequence analysis
tools



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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 299 AA (of which 8% low-complexity regions filtered out)

Date run: 2005-06-08 04:55:01 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

1,974,938 sequences; 640,866,274 total letters

UniProt Release 5.1 consists of: Swiss-Prot Release 47.1 of 24-May-2005: 181821 en
TrEMBL Release 30.1 of 24-May-2005: 1748002 entries

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[NiceBlast view](#)

[Printable view](#)

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

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<input type="checkbox"/>	sp	Q92MQ7 Y175_HELPJ Hypothetical protein JHP0161 precursor [JHP...	523	e-147
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<input type="checkbox"/>	tr	Q5EVH4 _CAMJR Major antigenic peptide PEB4 [CJE0699] [Campylob...	138	1e-31
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<input type="checkbox"/>	tr	Q65RG0	_MANSM	SurA protein [surA] [Mannheimia succiniciproduce...	69	1e-10
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<input type="checkbox"/>	tr	Q9CJM0	_PASMU	Hypothetical protein PM1979 [PM1979] [Pasteurell...	68	2e-10
<input type="checkbox"/>	tr	Q6HJ34	_BACHK	Protein export protein prsA (EC 5.2.1.8) [prsA] ...	68	2e-10
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<input type="checkbox"/>	tr	Q72D64	_DESVH	Peptidyl-prolyl cis-trans isomerase domain protei...	68	3e-10
<input type="checkbox"/>	tr	Q62ZT8	_BACLD	Putative PpiC-type peptidyl-prolyl cis-trans iso...	68	3e-10
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<input type="checkbox"/>	sp	Q02473	PRSA_LACPA	Foldase protein prsA precursor (EC 5.2.1.8)...	67	5e-10

Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
([Help](#)) (use ScanProsite for more details about PROSITE matches)

Profile hits	PPIC_PPIASE_2
Pfam hits	Rotanase

Submission	Matches on query sequence											Mat
	1	50	100	150	200	250						1
Y175_HELPY												
Y175_HELPJ												
Q7VJY7												
Q7H902												
CBF2_CAMJE												
Q5HVV4												
Q8YJG8												
Q8FYE8												
Q57AV6												
Q98G68												
Q74H76												
Q6NCG1												
Q92MJ8												
Q8XNR4												
Q97H89												
Q89XV8												
Q899G4												
Q5FQC9												
Q8UA55												
Q7CSN8												
Q607H8												
Q6SF25												
Q74RE7												
Q5HYH3												
PRSA_CLOTE												
Q6G5U1												
Q6G8Q7												
Q82UR3												
Q5UF05												
PRSA_THETN												
Q7NTX8												
Q62JM3												
Q63V26												
PRSA2_BACCR												
Q7P917												
PLP_RICPR												
Q6HM18												
PLP_RICCN												
Q63EK8												
Q73BY8												
Q68NG8												
Q74H77												
Q7MCX5												
PRSA_BACHD												
PRSA2_BACAN												
Q8XYL4												
Q7H5E8												
Q7VTH9												
Q74BG7												
Q7NTX1												
Q5LNL7												
Q5P6R8												
Q5L289												
Q87R77												
Q6HHN3												
Q60BE4												
Q4ZVM3												
Q9I2T8												
PRSA2_LISMF												
PRSA2_LISIN												
Q5WHU3												
Q8XYP3												
PRSA4_BACCR												
Q87YS8												
Q5QYK3												
Q6SHE5												
Q65LT4												
PRSA2_LISMO												
PPID_HAEDU												
Q5NYD2												
Q7NTM9												
PRSA1_BACAN												
Q6HMC8												
PRSA_BACSU												
Q63EV9												
Q8DG31												
Q67K72												
PRSA_OCEIH												
Q9KQT8												
PRSA1_BACCR												
Q8EG15												
Q7MMG3												
Q82SU8												
Q7NUZ4												
Q73CC1												
Q88KI6												

Alignments

sp P56112 Hypothetical protein HP0175 precursor [HP0175] 299
Y175_HELPY [Helicobacter pylori
(Campylobacter pylori)] AA
align

Score = 534 bits (1375), Expect = e-150
Identities = 275/299 (91%), Positives = 275/299 (91%)

Query: 1 MKKNILNLALVGALSTSFLMXXXXXXXXXXXXXXXXXXXXSSAGVLATVDGRPITKSDFDM 60
MKKNILNLALVGALSTSFLM DSSAGVLATVDGRPITKSDFDM
Sbjct: 1 MKKNILNLALVGALSTSFLMAKPAHNANNATHNTKTTDSSAGVLATVDGRPITKSDFDM 60

Query: 61 IKQRNPNFDFDKLXXXXXXALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE 120
IKQRNPNFDFDKL ALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE
Sbjct: 61 IKQRNPNFDFDKLKEKEKEALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE 120

Query: 121 FWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180
FWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ
Sbjct: 121 FWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180

Query: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAAAFALTPGDYTKTPV 240
PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAAAFALTPGDYTKTPV
Sbjct: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAAAFALTPGDYTKTPV 240

Query: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK 299
KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK
Sbjct: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK 299

sp Q9ZMQ7 Hypothetical protein JHP0161 precursor [JHP0161] 299
Y175_HELPJ [Helicobacter
pylori J99 (Campylobacter pylori J99)] AA
align

Score = 523 bits (1348), Expect = e-147
Identities = 268/299 (89%), Positives = 272/299 (90%)

Query: 1 MKKNILNLALVGALSTSFLMXXXXXXXXXXXXXXXXXXXXSSAGVLATVDGRPITKSDFDM 60
MKKNILNLALVGALS SFLM D+SAGVLATVDGRPITKSDFDM
Sbjct: 1 MKKNILNLALVGALSASFLMAKPAHNANNSTHNTKETTDASAGVLATVDGRPITKSDFDM 60

Query: 61 IKQRNPNFDFDKLXXXXXXALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE 120
IKQRNPNFDFDKL ALI+QAIRTALVENEAK EKL+ TPEFKAMMEAVKKQALVE
Sbjct: 61 IKQRNPNFDFDKLKEKEKEALIEQAIRTALVENEAKAEKLNQTPEFKAMMEAVKKQALVE 120

Query: 121 FWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180
FWAKKQAEVKK+QIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ
Sbjct: 121 FWAKKQAEVKKIQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180

Query: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAAAFALTPGDYTKTPV 240
PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAAAFALTPGDYTKTPV
Sbjct: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAAAFALTPGDYTKTPV 240

Query: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK 299
KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK

Sbjct: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOERMNQRIEELRKHAKIVINK 299

tr Q7VJY7 Hypothetical protein [HH0105] [Helicobacter hepaticus] 276 AA
 Q7VJY7_HELHP

align

Score = 225 bits (573), Expect = 1e-57

Identities = 121/258 (46%), Positives = 161/258 (61%), Gaps = 1/258 (0%)

Query: 42 AGVLATVDGRPITKSDFDIKQNRPNFDFDKLXXXXXXALIDQAIRALTALVENEAKTEKLD 101
 A ATVDG IT D +++KQ ENF+++KL LI++ I L+ AK EKLD

Sbjct: 20 AKTYATVDGVAITDKDMEILKQSIPNFYNKLSEQEKEMLINELINRQLILKAAKQEKLD 79

Query: 102 STPEFKAMMEAVKKQALVEFWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARH 161
 ++ E+ + ++K L++ W KKQA + + + +++ Y N+ + F+ QE ARH

Sbjct: 80 TSKEYTDTINSIKDNLIDLTWTKKQANSTQVPTMNDALRKIYQENEGE-FIDQEGKARH 138

Query: 162 ILVKTEDEAKRIIASEIDKQPKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAP 221
 ILVK+E EAK II E+DE KAK EAKTELAN +IDP SE +NGGDLG F++ M P

Sbjct: 139 ILVKSESEAKEIIKELDKVGKAKAEAKFIELANAKSIDPASKQKQNGGDLGVFKRAGMDP 198

Query: 222 DFSKAAFALTPGDYTKTPVKTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOER 281
 FSKAAF L PG YTK EV T+FGYHIIYL K P Y+ AK I+ ++ + Q

Sbjct: 199 MFSKAAFDLKPGTYTKEPVLTOFGYHIIYLERKSEPKVIPYKDAKKIENSIMQSIQGG 258

Query: 282 MNQRIEELRKHAKIVINK 299

M Q+I+ LR AKI I K

Sbjct: 259 MMQKIQALRAKAKIKITK 276

tr Q7M902 CELL BINDING FACTOR 2 MAJOR ANTIGEN PEB4A [WS1281] 271
 Q7M902_WOLSU [Wolinella succinogenes] AA
align

Score = 184 bits (466), Expect = 3e-45

Identities = 100/255 (39%), Positives = 152/255 (59%), Gaps = 7/255 (2%)

Query: 41 SAGVLATVDGRPITKSDFDIKQNRPNFDFDKLXXXXXXALIDQAIRALTALVENEAKTEKL 100
 SA LA+VDG IT D ++ + P +D+L +++QAI L+ +AK+E +

Sbjct: 21 SAKTLASVDGDEITDKDISVMLRAMPVGSYDQLPEDMQKKVLEQAIERKLLAKQAKSEGI 80

Query: 101 DSTPEFKAMMEAVKKQALVEFWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHAR 160
 ++ EFK +E K+ +E W ++Q K + E +M+ FY+ NK++ + A+

Sbjct: 81 QNSKEFKDALEDAKEDLTLEVWMRQOMNNAK---VSEGDMRKIFYDENKEKFVQPELVKAK 137

Query: 161 HILVKTEDEAKRIIASEIDKQPKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMA 220
 HILV+ E EAK +I+ET K AK KP EIA +IDP QNGG+LG F K+QM

Sbjct: 138 HILVQNEKEAKEVIAEIGKAG-AKASEKFSKAKSKSIDPAG---QNGGELGWFSKDQMV 193

Query: 221 PDFSKAAFALTPGDYTKTPVKTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOE 280
 P+P+ AAFAL G Y+KTPVKT+FGYH+IY K + YE KP I+ L+ + F++

Sbjct: 194 PEFANAALQKGSYSKTPVKTOFGYHVIYAEDKKAQAVLPYEDVKPQIEQNLKIQKFRD 253

Query: 281 RMNQRIEELRKHAKI 295

++ ++LR+ A++
Sbjct: 254 SVSSTAKKLREKAQV 268

sp Q46105 Cell binding factor 2 precursor (Major antigen pab4A) 273
CBF2_CAMJE [cbf2] AA
[Campylobacter jejuni] align

Score = 138 bits (348), Expect = 1e-31
Identities = 88/256 (34%), Positives = 137/256 (53%), Gaps = 6/256 (2%)

Query: 41 SAGVLATVDGRPITKSDF-DMIKQRNPNFDFDKLXXXXXXALIDQAIRTALVENEAKTEK 99
+A +ATV+G+ I+ ++ + DF L ALI Q I L+ +AK +
Sbjct: 20 NAATVATVNGKSISDTEVSEFFAPMLRGQDFKTLPDNQKKALIQQYIMQDLILQDAKKQN 79

Query: 100 LDSTPEFKAMMEAVKKQALVEFWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHA 159
L+ P + ++ K LV + +K +K I +++ FY+ NKD+ A
Sbjct: 80 LEKDPLYTKELDRAKDAILVNVYQEKILNTIK---IDAAKVKA FYDQNKDKYVKPARVQA 136

Query: 160 RHILVKTEDEAKRII SEIDKQPKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQM 219
+RIIV TE EAK II+E+ + +AKF ELA +IDF SKN GG+LG F ++ M
Sbjct: 137 KHILVATEKEAKDIINELKGLKGKELDAKFSELAKEKSIDPGSKN--QGGELGWFDQSTM 194

Query: 220 APDFSKAAAFALTPGDYTKTPVKTEFGYHIIYLISKDSPVTTYTYEQAKPTIKGMLQEKLFQ 279
F+ AAAL G T TEVKT EGYR+I + + +++ K I+ L+ + F+
Sbjct: 195 VKPFTDAAFALKNGTITTTTPVKTNFGYHVILKENSQAKGQIKFDEVKQGIENGLKFEEFK 254

Query: 280 ERMNQRIEELRKHAKI 295
+ +NQ+ ++L AK+
Sbjct: 255 KVINQKGQDLLNSAKV 270

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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name **EFTU_HELPJ**
 Primary accession number **Q9ZK19**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 39, May 2000
 Sequence was last modified in Release 39, May 2000
 Annotations were last modified in Release 47, May 2005

Name and origin of the protein

Protein name **Elongation factor Tu**
 Synonym **EF-Tu**
 Gene name

Name: tuf

Synonyms: tufA

OrderedLocusNames: JHP1128

From **Helicobacter pylori J99 (Campylobacter pylori J99)** [TaxID: 85963]

Taxonomy **Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales; Helicobacteraceae; Helicobacter.**

References

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

DOI=10.1038/16495; PubMed=9923682 [NCBI, ExPASy, EBI, Israel, Japan]

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Trust T.J.;

"Genomic sequence comparison of two unrelated isolates of the human gastric pathogen *Helicobacter pylori*.";
 Nature 397:176-180(1999).

Comments

- **FUNCTION:** This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis.
- **SUBUNIT:** Monomer (*By similarity*).
- **SUBCELLULAR LOCATION:** Cytoplasmic.
- **SIMILARITY:** Belongs to the GTP-binding elongation factor family. EF-Tu/EF-1A subfamily.

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the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

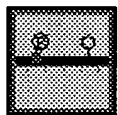
Cross-references

EMBL	AE001541; AAD06711.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	E71844; E71844.	
HSSP	P02990; 1ETU. [HSSP ENTRY / PDB]	
SMR	Q9ZK19; 5-399.	
CMR	Q9ZK19; JHP1128.	
HAMAP	MF_00118; -; 1. PBIL [Family / Alignment / Tree]	
InterPro	IPR004541; EF-Tu. IPR004160; EFTU_Cterm. IPR004161; EFTU_D2. IPR000795; ProtSyn_GTPbind. IPR005225; Small_GTP. Graphical view of domain structure.	
Pfam	PF00009; GTP_EFTU; 1. PF03144; GTP_EFTU_D2; 1. PF03143; GTP_EFTU_D3; 1. Pfam graphical view of domain structure.	
PRINTS	PR00315; ELONGATNFCT.	
TIGRFAMs	TIGR00485; EF-Tu; 1. TIGR00231; small_GTP; 1.	
PROSITE	PS00301; EFACTOR_GTP; 1.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOGENOM	[Family / Alignment / Tree]	
BLOCKS	Q9ZK19.	
ProtoNet	Q9ZK19.	
ProtoMap	Q9ZK19.	
PRESAGE	Q9ZK19.	
DIP	Q9ZK19.	
ModBase	Q9ZK19.	
SWISS-2DPAGE	Get region on 2D PAGE.	
UniRef	View cluster of proteins with at least 50% / 90% identity.	

Keywords

Complete proteome; Elongation factor; GTP-binding; Protein biosynthesis.

Features



Feature table viewer

Key	From	To	Length	Description
NP_BIND	19	26	8	GTP (By similarity).
NP_BIND	81	85	5	GTP (By similarity).
NP_BIND	136	139	4	GTP (By similarity).

Sequence information

Length: **399** Molecular weight: **43730** CRC64: **4E72A877BFCD104B** [This is a checksum on the AA Da sequence]

```

      10      20      30      40      50      60
MAKEKFNRTN PHVNIGTIGH VYHGKTTLSA AISAVLSLKG LAEMKDYDNI DNAPQEKERG

      70      80      90     100     110     120
ITIATSHIEY ETETRHYAHV DCPGHADYVK NMITGAAQMD GAILVVSAAAD GPMPQTREHI

     130     140     150     160     170     180
LLSRQVGVPVH IVVFLNKQDM VDDQELLELV EMEVRELLSA YEFPGDDTPI VAGSALRALE

     190     200     210     220     230     240
EAKAGNVGEW GEKVLKLMAE VDSYIPTPER DTEKTFLMPV EDVFSIAGRG TVVTGRIERG

     250     260     270     280     290     300
VVKVGDEVEI VGIRATQKTT VTGVEMFRKE LEKGEAGDNV GVLLRGTKKE EVERGMVLCK

     310     320     330     340     350     360
PGSITPHKKF EEEIYVLSKE EGGRHTPFFT NYRPQFYVRT TDVTGSITLP EGVEMVMPGD

     370     380     390
NVKITVELIS PVALELGTKF AIREGGRTVG AGVVSNIIE

```

Q9ZK19 in FASTA
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ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)




ScanProsite, MotifScan



Submit a homology modeling request to SWISS-
MODEL



NPSA Sequence analysis
tools

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In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 399 AA (of which 5% low-complexity regions filtered out)

Date run: 2005-06-08 05:58:30 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

1,974,938 sequences; 640,866,274 total letters

UniProt Release 5.1 consists of: Swiss-Prot Release 47.1 of 24-May-2005: 181821 en

TrEMBL Release 30.1 of 24-May-2005: 1748002 entrie

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List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db	AC	Description	Score	E-value
<input checked="" type="checkbox"/>	sp	Q9ZK19 EFTU_HELPJ Elongation factor Tu (EF-Tu) [tuf] [Helicob...	743	0.0
<input checked="" type="checkbox"/>	sp	P56003 EFTU_HELPY Elongation factor Tu (EF-Tu) [tuf] [Helicob...	728	0.0
<input type="checkbox"/>	tr	Q7VJ74 _HELHP Translation elongation factor EF-Tu (EC 3.6.1.48...	680	0.0
<input checked="" type="checkbox"/>	sp	P42482 EFTU_WOLSU Elongation factor Tu (EF-Tu) [tuf] [Wolinel...	667	0.0
<input checked="" type="checkbox"/>	sp	Q69303 EFTU_CAMJE Elongation factor Tu (EF-Tu) [tuf] [Campylo...	637	0.0
<input checked="" type="checkbox"/>	tr	Q5HVZ7 _CAMJR Translation elongation factor Tu [tuf] [Campylob...	637	0.0
<input checked="" type="checkbox"/>	sp	P64027 EFTU_NEIMB Elongation factor Tu (EF-Tu) [tufA] [Neisse...	578	e-164
<input checked="" type="checkbox"/>	sp	P64026 EFTU_NEIMA Elongation factor Tu (EF-Tu) [tufA] [Neisse...	578	e-164
<input type="checkbox"/>	tr	Q748X8 _GEOSL Translation elongation factor Tu [tuf-2] [Geobac...	575	e-163
<input type="checkbox"/>	tr	Q5F5Q8 _NEIG1 Translation elongation factor TU [NGO1842] [Neis...	575	e-163

<input type="checkbox"/>	tr	Q839G8	_ENTFA Translation elongation factor Tu [tuf] [Enteroco...	575	e-163
<input type="checkbox"/>	tr	Q5NID9	_FRATT Elongation factor Tu (EF-Tu) [tufA] [Francisella...	574	e-162
<input type="checkbox"/>	sp	Q8XGZ0	EFTU_RALSO Elongation factor Tu (EF-Tu) [tufA] [Ralsto...	573	e-162
<input type="checkbox"/>	tr	Q7M7F1	_CHRVO Translation elongation factor Tu (EC 3.6.1.48) [...]	573	e-162
<input checked="" type="checkbox"/>	sp	Q50306	EFTU_BACST Elongation factor Tu (EF-Tu) [tuf] [Bacillu...	571	e-162
<input type="checkbox"/>	tr	Q5L3Z9	_GEOKA Translation elongation factor Tu (EF-Tu) [tufA] ...	570	e-161
<input type="checkbox"/>	tr	Q5P334	_AZOSE Elongation factor Tu [tufB] [Azoarcus sp. (strai...	569	e-161
<input type="checkbox"/>	sp	Q8R7T8	EFTU2_THETN Elongation factor Tu-B (EF-Tu-B) [tufB] [T...	568	e-161
<input type="checkbox"/>	sp	Q8R603	EFTU_FUSNN Elongation factor Tu (EF-Tu) [tuf] [Fusobac...	568	e-160
<input type="checkbox"/>	tr	Q63PZ6	_BURPS Elongation factor Tu [tufA1] [Burkholderia pseud...	568	e-160
<input type="checkbox"/>	tr	Q62GK3	_BURMA Translation elongation factor Tu [tuf-1] [Burkho...	568	e-160
<input type="checkbox"/>	sp	P42481	EFTU_THICU Elongation factor Tu (EF-Tu) [tuf] [Thiobac...	567	e-160
<input type="checkbox"/>	sp	P48864	EFTU_NEIGO Elongation factor Tu (EF-Tu) [tuf] [Neisser...	567	e-160
<input type="checkbox"/>	sp	Q8R7V2	EFTU1_THETN Elongation factor Tu-A (EF-Tu-A) [tufA] [T...	567	e-160
<input type="checkbox"/>	tr	Q83ES6	_COXBU Translation elongation factor Tu [tuf-2] [Coxiel...	567	e-160
<input type="checkbox"/>	tr	Q7P364	_FUSNV Protein translation elongation factor Tu (EF-TU)...	567	e-160
<input type="checkbox"/>	tr	Q7TTF9	_HAEDU Elongation factor tu, EF-Tu [tufA] [Haemophilus ...]	567	e-160
<input type="checkbox"/>	sp	Q99QM0	EFTU_CAUCR Elongation factor Tu (EF-Tu) [tufA] [Caulob...	566	e-160
<input type="checkbox"/>	sp	Q8Y422	EFTU_LISMO Elongation factor Tu (EF-Tu) [tuf] [Listeri...	566	e-160
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<input type="checkbox"/>	sp	Q927I6	EFTU_LISIN Elongation factor Tu (EF-Tu) [tuf] [Listeri...	566	e-160
<input type="checkbox"/>	tr	Q81ZS3	_NITEU GTPases-translation elongation factors and sulfa...	565	e-160
<input type="checkbox"/>	sp	P57939	EFTU1_PASMU Elongation factor Tu-A (EF-Tu-A) [tufA] [P...	565	e-160
<input type="checkbox"/>	tr	Q65QG6	_MANSM TufB protein [tufB] [Mannheimia succiniciproduce...	565	e-160
<input type="checkbox"/>	tr	Q8L160	_MYXXA Elongation factor Tu [tufA] [Myxococcus xanthus]	565	e-160
<input type="checkbox"/>	tr	Q5FTY1	_GLUOX Protein Translation Elongation Factor Tu (EF-TU)...	564	e-159
<input type="checkbox"/>	sp	Q8ETY4	EFTU_OCEIH Elongation factor Tu (EF-Tu) [tuf] [Oceanob...	564	e-159
<input type="checkbox"/>	tr	Q605B0	_METCA Translation elongation factor Tu [tuf-2] [Methyl...	563	e-159
<input type="checkbox"/>	tr	Q8EK70	_SHEON Translation elongation factor Tu [tufA] [Shewane...	563	e-159
<input type="checkbox"/>	tr	Q7TT91	_BORPE Elongation factor Tu [tufA] [Bordetella pertussis]	563	e-159
<input type="checkbox"/>	tr	Q79GC6	_BORPA Elongation factor Tu [tuf] [Bordetella parapertu...	563	e-159
<input type="checkbox"/>	tr	Q79G84	_BORBR Elongation factor Tu [tuf] [Bordetella bronchise...	563	e-159
<input type="checkbox"/>	tr	Q5GWR8	_XANOR Elongation factor Tu [tufB] [Xanthomonas oryzae ...]	563	e-159
<input type="checkbox"/>	sp	P43926	EFTU_HAEIN Elongation factor Tu (EF-Tu) [tufA] [Haemop...	562	e-159
<input type="checkbox"/>	sp	P57966	EFTU2_PASMU Elongation factor Tu-B (EF-Tu-B) [tufB] [P...	561	e-159
<input type="checkbox"/>	tr	Q65PA9	_BACLD TufA (Elongation factor Tu) [tufA] [Bacillus lic...	561	e-159
<input type="checkbox"/>	sp	P33169	EFTU_SHEPU Elongation factor Tu (EF-Tu) [tuf] [Shewane...	561	e-158
<input type="checkbox"/>	tr	Q8EK81	_SHEON Translation elongation factor Tu [tufB] [Shewane...	561	e-158
<input type="checkbox"/>	tr	Q5NQ65	_ZYMOM Translation elongation factor [ZMO0516] [Zymomon...	561	e-158
<input type="checkbox"/>	sp	Q8CQ81	EFTU_STAEP Elongation factor Tu (EF-Tu) [tuf] [Staphyl...	560	e-158
<input type="checkbox"/>	sp	P33167	EFTU_BURCE Elongation factor Tu (EF-Tu) [tuf] [Burkhol...	560	e-158
<input type="checkbox"/>	tr	Q5HRK4	_STAEQ Translation elongation factor Tu [tuf] [Staphylo...	560	e-158
<input type="checkbox"/>	sp	Q929L6	EFTU_BACHD Elongation factor Tu (EF-Tu) [tuf] [Bacillu...	560	e-158
<input type="checkbox"/>	sp	Q8NL22	EFTU_XANAC Elongation factor Tu (EF-Tu) [tufA] [Xantho...	560	e-158
<input type="checkbox"/>	sp	P33166	EFTU_BACSU Elongation factor Tu (EF-Tu) (P-40) [tuf] [...]	560	e-158

<input type="checkbox"/>	sp	P64029	EFTU_STAAB	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...	559	e-158
<input type="checkbox"/>	sp	Q6GBT9	EFTU_STAAS	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...	559	e-158
<input type="checkbox"/>	sp	Q6GJC0	EFTU_STAAR	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...	559	e-158
<input type="checkbox"/>	sp	P99152	EFTU_STAAN	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...	559	e-158
<input type="checkbox"/>	sp	P64028	EFTU_STAAM	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...	559	e-158
<input type="checkbox"/>	tr	Q5HIC7	_STAAC	Translation elongation factor Tu	[tuf]	[Staphylo...	559	e-158
<input type="checkbox"/>	tr	Q5QWA3	_IDILO	Translation elongation factor EF-Tu	[tufB_1]	[Id...	559	e-158
<input type="checkbox"/>	tr	Q6N4Q4	_RHOPA	Elongation factor Tu (EC 3.6.1.48)	[tuf/ EF-Tu]	...	558	e-158
<input type="checkbox"/>	tr	Q73F98	_BACC1	Translation elongation factor Tu	[tuf]	[Bacillus...	558	e-158
<input type="checkbox"/>	sp	Q814C4	EFTU_BACCR	Elongation factor Tu (EF-Tu)	[tuf]	[Bacillu...	558	e-158
<input type="checkbox"/>	sp	Q81VT2	EFTU_BACAN	Elongation factor Tu (EF-Tu)	[tuf]	[Bacillu...	558	e-158
<input type="checkbox"/>	tr	Q6HPR0	_BACHK	Protein-synthesizing GTPase (Translation elongat...			558	e-158
<input type="checkbox"/>	tr	Q63H92	_BACCZ	Protein-synthesizing GTPase (Translation elongat...			558	e-158
<input type="checkbox"/>	tr	Q6MJ00	_BDEBA	Translation elongation factor Tu (EC 3.6.1.48)	[...]		557	e-157
<input type="checkbox"/>	tr	Q9F9S8	_9PROT	Eftu [eftu] [EDTA-degrading bacterium BNC1]			557	e-157
<input type="checkbox"/>	tr	Q5PIW4	_SALPA	Elongation factor Tu [tufA] [Salmonella paratyph...			556	e-157
<input type="checkbox"/>	tr	Q57H76	_SALCH	Protein chain elongation factor EF-Tu (Duplicate...			556	e-157
<input type="checkbox"/>	tr	Q6N0C2	_9PROT	EF-Tu [orf3309] [Magnetospirillum gryphiswaldense]			556	e-157
<input type="checkbox"/>	sp	P26184	EFTU_FLESI	Elongation factor Tu (EF-Tu)	[tuf]	[Flexist...	556	e-157
<input type="checkbox"/>	sp	Q83JC4	EFTU_SHIFL	Elongation factor Tu (EF-Tu)	[tufA]	[Shigel...	555	e-157
<input type="checkbox"/>	sp	P0A6N1	EFTU_ECOLI	Elongation factor Tu (EF-Tu) (P-43)	[tufA]	...	555	e-157
<input type="checkbox"/>	sp	P0A6N2	EFTU_ECOL6	Elongation factor Tu (EF-Tu) (P-43)	[tufA]	...	555	e-157
<input type="checkbox"/>	sp	P0A6N3	EFTU_ECO57	Elongation factor Tu (EF-Tu) (P-43)	[tufA]	...	555	e-157
<input type="checkbox"/>	tr	Q5ZYP5	_LEGPH	Translation elongation factor Tu (EF-Tu) (EC 3.6...			555	e-157
<input type="checkbox"/>	tr	Q5X873	_LEGPA	Translation elongation factor Tu [tufA] [Legione...			555	e-157
<input type="checkbox"/>	tr	Q57J27	_SALCH	Protein chain elongation factor EF-Tu (Duplicate...			555	e-157
<input type="checkbox"/>	sp	P0A1H5	EFTU_SALTY	Elongation factor Tu (EF-Tu)	[tufA]	[Salmon...	555	e-157
<input type="checkbox"/>	sp	P0A1H6	EFTU_SALTI	Elongation factor Tu (EF-Tu)	[tufA]	[Salmon...	555	e-157
<input type="checkbox"/>	sp	O31298	EFTU_BUCAP	Elongation factor Tu (EF-Tu)	[tuf]	[Buchner...	555	e-157
<input type="checkbox"/>	tr	Q6FZC0	_BARQU	Elongation factor tu (EF-tu)	[tuf1]	[Bartonella ...]	555	e-157
<input type="checkbox"/>	tr	Q5WZL4	_LEGPL	Elongation factor Tu [tufA] [Legionella pneumoph...			555	e-157
<input type="checkbox"/>	sp	Q925Y6	EFTU_RHIME	Elongation factor Tu (EF-Tu)	[tufA]	[Rhizob...	554	e-156
<input type="checkbox"/>	tr	Q6FZL2	_BARQU	Elongation factor tu (EF-tu)	[tuf2]	[Bartonella ...]	554	e-156
<input type="checkbox"/>	tr	Q7MYE8	_PHOLL	Elongation factor Tu (EF-Tu)	[tufA]	[Photorhabdu...	554	e-156
<input type="checkbox"/>	sp	P18668	EFTU_SYNP6	Elongation factor Tu (EF-Tu)	[tuf]	[Synecho...	554	e-156
<input type="checkbox"/>	sp	O31297	EFTU_BUCAI	Elongation factor Tu (EF-Tu)	[tuf]	[Buchner...	554	e-156
<input type="checkbox"/>	sp	P33165	EFTU_BACFR	Elongation factor Tu (EF-Tu)	[tuf]	[Bactero...	553	e-156
<input type="checkbox"/>	sp	P33171	EFTU_SYNP7	Elongation factor Tu (EF-Tu)	[tuf]	[Synecho...	553	e-156
<input type="checkbox"/>	sp	Q8ZAN8	EFTU2_YERPE	Elongation factor Tu-B (EF-Tu-B)	[tufB]	[Y...	553	e-156
<input type="checkbox"/>	tr	Q66FQ9	_YERPS	Elongation factor Tu [tufA] [Yersinia pseudotube...			553	e-156
<input type="checkbox"/>	tr	Q8KHX9	_BARHE	Elongation factor TU (EF-Tu)	[tufB]	[Bartonella ...]	552	e-156
<input type="checkbox"/>	tr	Q89J82	_BRAJA	Elongation factor TU [tuf]		[Bradyrhizobium japon...	552	e-156
<input type="checkbox"/>	tr	Q727D5	_DESVH	Translation elongation factor Tu [tuf]		[Desulfov...	552	e-156
<input type="checkbox"/>	tr	Q7N9B1	_PHOLL	Translation elongation factor EF-Tu.B	[tufB]	[Ph...	552	e-156
<input type="checkbox"/>	sp	Q8UE16	EFTU_AGRT5	Elongation factor Tu (EF-Tu)	[tufA]	[Agroba...	551	e-156

Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
([Help](#)) (use ScanProsite for more details about PROSITE matches)

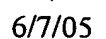
Profile hits

Pfam hits

GTP_EFTU

GTP_EFTU_D2

GTP_EFTU_D3



Alignments

sp Q9ZK19 Elongation factor Tu (EF-Tu) [tuf] [Helicobacter pylori] 399
 EFTU_HELPJ J99 AA
 (Campylobacter pylori J99)] align

Score = 743 bits (1919), Expect = 0.0
 Identities = 378/399 (94%), Positives = 378/399 (94%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG
 Sbjct: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
 Sbjct: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVPPIVFLNK SAYEFPGDDTPIVAGSALRALE
 Sbjct: 121 LLSRQVGVPPIVFLNKQDMVDDQELLELVEMEVRELLSAYEFPGDDTPIVAGSALRALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG
 Sbjct: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK
 Sbjct: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD
 Sbjct: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE
 Sbjct: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

sp P56003 Elongation factor Tu (EF-Tu) [tuf] [Helicobacter pylori] 399 AA
 EFTU_HELPY (Campylobacter pylori)] align

Score = 728 bits (1880), Expect = 0.0
 Identities = 371/399 (92%), Positives = 373/399 (92%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKFNRT PHVNIGTIGHV HGKTTLSAAISAVLSLKGLAEMKDYNIDNAP+EKERG
 Sbjct: 1 MAKEKFNRTKPHVNIGTIGHVDHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITIATSHIEYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
 Sbjct: 61 ITIATSHIEYETENRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVPPIVFLNK SAYEFPGDDTPIVAGSALRALE

Sbjct: 121 LLSRQVGVP HIVVFLNKQDMVDDQELLELVEMEVRELLSAYEFPGDDTPIVAGSALRALE 180

Query: 181 EAKAGNVGEWGEKVLKILMAEVD SYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG 240
EAKAGNVGEWGEKVLKILMAEVD+YIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG

Sbjct: 181 EAKAGNVGEWGEKVLKILMAEVDAYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
VVKVGDEVEIVGIR TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK

Sbjct: 241 VVKVGDEVEIVGIRPTQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYPQFYVRTT DVTGSITLPEGVEMVMPGD 360
PGSITPHKKFE EIIYVLSKEEGGRHTPFFTNYPQFYVRTT DVTGSITLPEGVEMVMPGD

Sbjct: 301 PGSITPHKKFEGEIIYVLSKEEGGRHTPFFTNYPQFYVRTT DVTGSITLPEGVEMVMPGD 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE

Sbjct: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

tr Q7VJ74 Translation elongation factor EF-Tu (EC 3.6.1.48) [tufA] 399 AA
Q7VJ74_HELHP [Helicobacter hepaticus]

align

Score = 680 bits (1755), Expect = 0.0
Identities = 341/399 (85%), Positives = 360/399 (89%)

Query: 1 MAKEKFNRTNPHVNI GTIGHVYHGKTTLSAAISAVLSLKGLAEMKD YDNIDNAPQEKERG 60
MAKEKF + PHVN+GTIGHV HGKTTLSAAISAVL+ KGLAE+KDYDNIDNAP+EKERG

Sbjct: 1 MAKEK FVKNKPHVNVGTIGHVDHGKTTLSAAISAVLATKGLAELKD YDNIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILLVSAADGMPQ TREHI 120
ITIATSHIEYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILLVSAADGMPQ TREHI

Sbjct: 61 ITIATSHIEYETENRHYAHVDCPGHADYVKNMITGAAQMDGAILLVSAADGMPQ TREHI 120

Query: 121 LLSRQVGVP HIVVFLNKXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
LLSRQVG V +IVVFLNK S Y+FPGDDTPT+AGSAL+ALE

Sbjct: 121 LLSRQVG VHYIVVFLNKQDMVDDAEELLELVEMEVRELLS QYDFPGDDTPIIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKILMAEVD SYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG 240
EAKAGNVGEWGEKVLKIM EVD YIPT+RDEKTFILMPVEDVFSIAGRGT VVTGR+ERG

Sbjct: 181 EAKAGNVGEWGEKVLKILMEEVDKYIPTPQRDTEKTFILMPVEDVFSIAGRGT VVTGRVERG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
VV+VGDEVEIVGIR TQKTTVTGVEMFRKEL+KGEAGDNVG+LLRGTKKEEVERGMVLCK

Sbjct: 241 VVQVGDEVEIVGIRDTQKTTVTGVEMFRKELDKGEAGDNVGILLRGTKKEEVERGMVLCK 300

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYPQFYVRTT DVTGSITLPEGVEMVMPGD 360
PGSITPHKKFE EIIYVLSK+EGGRHTPEF YRQFYVRTT DVTGSI LP GVEMVMPGD

Sbjct: 301 PGSITPHKKFEGEIIYVLSKDEGGRTHPFFNGYRPFYVRTT DVTGSIELPSGVEMVMPGD 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
NVKITVELI+PVALE GT+FAIREGGRTVG+GVV+ IIE

Sbjct: 361 NVKITVELIAPVALEDGTRFAIREGGRTVGSGVVTKIIE 399

sp P42482 Elongation factor Tu (EF-Tu) [tuf] [Wolinella
EFTU_WOLSU succinogenes]

399
AA
align

Score = 667 bits (1720), Expect = 0.0
Identities = 337/397 (84%), Positives = 353/397 (88%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MAKEKF + PHVNIGTIGHV HGKTTLSAAISAVL+ KGL E+KDYD IDNAP+E+ERG
Sbjct: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120
        ITIATSHIEYETE RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI
Sbjct: 61  ITIATSHIEYETENRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LLSRQVGVP+IVVFLNK S Y+FFGDDTPIVAGSAL+ALE
Sbjct: 121  LLSRQVGVPPIVFLNKKEDMVDDAELLELVEMEIRELLSSYDFPGDDTPIVAGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
        EAK GNVGEWGEKVLKLM AEVD YIPTPERD +K FILMPVEDVFSIAGRGTVVTGRIERG
Sbjct: 181  EAKTGNVGEWGEKVLKLM AEVDRIYIPTPERDVDPFLMPVEDVFSIAGRGTVVTGRIERG 240

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        VVKVGDEVEIVGIR TQKTTVTGVEMFRKEL+KGEAGDNVGVLLRGTKKE+VERGMVLCK
Sbjct: 241  VVKVGDEVEIVGIRNTQKTTVTGVEMFRKELDKGEAGDNVGVLLRGTKKEDVERGMVLCK 300

Query: 301  PGSITPHKKFEEEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTVTSITLPEGVEMVMPGD 360
        GSTPH FE E+YVLSKEEGGRHTPEE YRPQFYVRTTDTVTSI+LPEGVEMVMPGD
Sbjct: 301  IGSITPHTNFEGEVYVLSKEEGGRHTPFFNGYRPFYVRTTDTVTSISLPEGVEMVMPGD 360

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
        NVKI VELI+PVALE GT+FAIREGGRTVGAGVV+ I
Sbjct: 361  NVKINVELIAPVALEEGTRFAIREGGRTVGAGVVTKI 397

```

sp O69303 Elongation factor Tu (EF-Tu) [tuf] [Campylobacter jejuni] 399 AA
EFTU_CAMJE

align

Score = 637 bits (1644), Expect = 0.0
Identities = 315/399 (78%), Positives = 350/399 (86%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MAKEKF+R PHVNIGTIGHV HGKTTLSAAISAVLS +GLAE+KDYDNIDNAP+EKERG
Sbjct: 1  MAKEKFSRNKPHVNIGTIGHVYHGKTTLSAAISAVLSRRGLAELKDYDNIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120
        ITIATSHIEYET+ RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI
Sbjct: 61  ITIATSHIEYETDNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LLSRQVGVP+IVVF+NK S+Y+FFGDDTPI++GSAL+ALE
Sbjct: 121  LLSRQVGVPPIVFMNKADMVDDAELLELVEMEIRELLSSYDFPGDDTPIISGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
        EAKAG GEW K++ LMA VDSYIPTP RDTK FILMP+EDVFSI+GRGTVVTGRIE+G

```

Sbjct: 181 EAKAGQDGEWSAKIMDLMAAVDSYIPTPTRDTEKDFLMPIEDVFSISGRGTVVVTGRIEKG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 VVKVGD +EIVGI+ TQ TTVTGVEMFRKE+++GEAGDNVGVLLRGTKKEEV RGMVL K

Sbjct: 241 VVKVGDTIEIVGIKDTQTTTVTGVEMFRKEMDQGEAGDNVGVLLRGTKKEEVIRGMVLAK 300

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
 P SITPH FE E+Y+L+K+EGGRHTPFF NYRPQFYVRTTDDVTGSI L +GVEMVMPG+

Sbjct: 301 PKSITPHTDFAEVIILNKDEGGRHTPFFFNRYRPQFYVRTTDDVTGSIKLADGVEMVMPGE 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV+ITV LI+PVALE GT+FAIREGG+TVG+GVVS II+

Sbjct: 361 NVRITVSLIAPVALEEGTRFAIREGGKTVGSGVVSIIK 399

tr Q5HVZ7 Translation elongation factor Tu [tuf] [Campylobacter] 399
 Q5HVZ7_CAMJR jejuni AA
 (strain RM1221) align

Score = 637 bits (1644), Expect = 0.0
 Identities = 315/399 (78%), Positives = 350/399 (86%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAKEKF+R PHVNIGTIGHV HGKTTL+AAISAVLS +GLAE+KDYDNIDNAP+EKERG

Sbjct: 1 MAKEKFSRNKPHVNIGTIGHVDHGKTTLTAAISAVLSRRGLAELKDYDNIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITIATSHIEYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI

Sbjct: 61 ITIATSHIEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVF+NK S+Y+FPGDDTPI++GSAL+ALE

Sbjct: 121 LLSRQVGVPPIVFMNKADMVDDAELELVEMEIRELLSSYDFPGDDTPIISGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVVTGRIERG 240
 EAKAG GEW K++ LMA VDSYIPTP RTEK FIMP+EDVFSI+GRGTVVVTGRIE+G

Sbjct: 181 EAKAGQDGEWSAKIMDLMAAVDSYIPTPTRDTEKDFLMPIEDVFSISGRGTVVVTGRIEKG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 VVKVGD +EIVGI+ TQ TTVTGVEMFRKE+++GEAGDNVGVLLRGTKKEEV RGMVL K

Sbjct: 241 VVKVGDTIEIVGIKDTQTTTVTGVEMFRKEMDQGEAGDNVGVLLRGTKKEEVIRGMVLAK 300

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
 P SITPH FE E+Y+L+K+EGGRHTPFF NYRPQFYVRTTDDVTGSI L +GVEMVMPG+

Sbjct: 301 PKSITPHTDFAEVIILNKDEGGRHTPFFFNRYRPQFYVRTTDDVTGSIKLADGVEMVMPGE 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV+ITV LI+PVALE GT+FAIREGG+TVG+GVVS II+

Sbjct: 361 NVRITVSLIAPVALEEGTRFAIREGGKTVGSGVVSIIK 399

sp P64027 Elongation factor Tu (EF-Tu) [tufA] [Neisseria] 394
 EFTU_NEIMB meningitidis AA
 (serogroup B) align

Score = 578 bits (1490), Expect = e-164
Identities = 284/398 (71%), Positives = 331/398 (82%), Gaps = 5/398 (1%)

```
Query: 1  MAKEKFNRRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAKEKF R+ PHVN+GTIGHV HGKTTL+AA++ +L+ K      K YD IDNAP+EK RG
Sbjct: 1  MAKEKFERSKPHVNVGTIGHVDHGKTTTLTAALTTLAKKFGGAAYDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI TSH+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 61  ITINTSHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+I+VF+NK      S+Y+EPGDD PIV GSAL+ALE
Sbjct: 121  LLARQVGVPYIIIVFMNKCVMDDAELELVEMEIRDLLSSYDFPGDDCPIVQGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
      A      + EK+ +L A +DSYIPTPER +K FL+P+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181  GDAA-----YEEKIFELAAALDSYIPTPERAVDKPFLLPIDVFSISGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300
      ++ VGDE+ELVG++ TQKTT TGVEMFRK L++G+AGDNVGVLLRGTKE+E+VERG VL K
Sbjct: 236  IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLDEGQAGDNVGVLLRGTKEEDVERGQVLAK 295

Query: 301  PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPOFYVRTTDTVTSITLPEGVEMVMPGD 360
      PG+ITPH KF+ E+YVLSKEEGGRHTPFF NYRPOFY RTTDTVTS++TL EGVEMVMPG+
Sbjct: 296  PGTITPHTKFAEVYVLSKEEGGRHTPFFFANYRPOFYFRTTDTVTGAVTLEEGVEMVMPGE 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      NV ITVELI+P+A+E G +FAIREGGRTVGAGVVS++I
Sbjct: 356  NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVVSNI 393
```

sp P64026 **Elongation factor Tu (EF-Tu) [tufA] [Neisseria** 394
EFTU_NEIMA **meningitidis** AA
 (serogroup A)] align

Score = 578 bits (1490), Expect = e-164
Identities = 284/398 (71%), Positives = 331/398 (82%), Gaps = 5/398 (1%)

```
Query: 1  MAKEKFNRRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAKEKF R+ PHVN+GTIGHV HGKTTL+AA++ +L+ K      K YD IDNAP+EK RG
Sbjct: 1  MAKEKFERSKPHVNVGTIGHVDHGKTTTLTAALTTLAKKFGGAAYDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI TSH+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 61  ITINTSHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+I+VF+NK      S+Y+EPGDD PIV GSAL+ALE
Sbjct: 121  LLARQVGVPYIIIVFMNKCVMDDAELELVEMEIRDLLSSYDFPGDDCPIVQGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
      A      + EK+ +L A +DSYIPTPER +K FL+P+EDVEST+GRGTVVTGR+ERG
Sbjct: 181  GDAA-----YEEKIFELAAALDSYIPTPERAVDKPFLLPIDVFSISGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300
```

```

      ++ VGDE+ELVG++ TQNTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VL K
Sbjct: 236 IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLDEGQAGDNVGVLLRGTKREDVERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPOFYVRTTDTVGSITLPEGVEMVMPGD 360
      PG+ITPH KP+ E+YVLSKEEGGRHTPFF NYRPOFY RTTDTG++TL EGVEMVMPG+
Sbjct: 296 PGTITPHTKFKAEVYVLSKEEGGRHTPFFANYRPOFYFRTTDTGAVTLEEGVEMVMPGE 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      NV ITVELI+P+A+E G +FAIREGGRTVGAGVVS++I
Sbjct: 356 NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVVSSVI 393

```

```

tr Q748X8      Translation elongation factor Tu [tuf-2] [Geobacter      396
  Q748X8_GEOSL sulfurreducens]      AA
                                         align

```

Score = 575 bits (1482), Expect = e-163
 Identities = 285/400 (71%), Positives = 328/400 (81%), Gaps = 5/400 (1%)

```

Query: 1  MAKEKFNRNTNPVHNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK KP RT PHVNIQTIGHV HGKTTL+AAI+ VL+ +G AE + +D IDNAP+E+ERG
Sbjct: 1  MAKAKFERTKPHVHNIGTIGHVDHGKTTLTAAITKVLAERGQAEFRGFDQIDNAPEERERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITIATSH+EYETE RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 61  ITIATSHVEYETEKRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+IVVFLNK S+Y+FPGDD PI+ GSAL+ L
Sbjct: 121  LLARQVGVPYIVVFLNKADMVDDEELLELEIRELLSSYDFPGDDIPIIKGSALKGLN 180

Query: 181  EAKAGNVGEWGEK-VLKLMAEVD SYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIER 239
      G+ E GE+ +LKLM VD+YIP PER +K FLMPVEDVFSI+GRGTV TGR+ER
Sbjct: 181  ----GDKDELGEEAILKLMEAVDNYIPEPERAVDKPFLMPVEDVFSISGRGTVATGRVER 236

Query: 240  GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      G+VKVG+EVEIVGI+AT KTTVTGVEMFRK L++G AGDN+G LLRG K+E++ERG VL
Sbjct: 237  GIVKVGEEVEIVGIKATAKTTVTGVEMFRKLLDEGRAGDNIGALLRGVKREDIERGQVLA 296

Query: 300  KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPOFYVRTTDTVGSITLPEGVEMVMPG 359
      KPGSITPH KP+ E Y+L+KEEGGRHTPFF YRPQFY RTTDTG + LP G EMVMPG
Sbjct: 297  KPGSITPHTKFKAEAYILTKEEGGRHTPFFNGYRPOFYFRTTDTGVVDLPAGTEMVMPG 356

Query: 360  DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNV +T+ LI+P+A++ G +FAIREGGRTVGAGVVS+ILE
Sbjct: 357  DNVAVTINLITPIAMDEGLRFAIREGGRTVGAGVVSSIIE 396

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tr Q5F5Q8      Translation elongation factor TU [NGO1842] [Neisseria      394
  Q5F5Q8_NEIG1 gonorrhoeae      AA
      (strain ATCC 700825 / FA 1090)]      align

```

Score = 575 bits (1482), Expect = e-163
 Identities = 282/398 (70%), Positives = 330/398 (82%), Gaps = 5/398 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MAKEKF R+ PHVN+GTIGHV HGKTTL+AA++ +L+ K      K YD IDNAP+EK RG
Sbjct: 1  MAKEKFSRKHVNIGTIGHVDHGKTTLTAALTILAKKFGGAAYDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
        ITI TSH+EYETETRHYAHVDCPGHADVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 61  ITINTSHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LL+RQVGVP+I+VF+NK                      S+Y+FGDD PIV GSAL+ALE
Sbjct: 121  LLARQVGVPYIIVFMNKCDDAELELLELVEMEIRDLLSSYDFPGDDCPVQGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVVTGRIERG 240
        A      + EK+ +L +DSYIPTER +K FL+P+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181  GDAA-----YEEKIFELATALDSYIPTPERAVDKPFLLPIDVFSISGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        ++ VGDE+EIVG++ TQKTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VL K
Sbjct: 236  IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLDEGQAGDNVGVLLRGTKREDVERGQVLAK 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
        PG+ITPH KF+ E+YVLSKEEGGRHTPF FT NYRPQFY RTTDTVTG++TL +GVEMVMPG+
Sbjct: 296  PGTITPHTKFKAENVVLSKEEGGRHTPFFANYRPQFYFRTTDTVTGAVTLEKGVEMVMPGE 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
        NV ITVELI+P+A+E G +FAIREGGRTVGAGVVS++I
Sbjct: 356  NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVSSVI 393

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tr Q839G8      Translation elongation factor Tu [tuf] [Enterococcus 395
      Q839G8_ENTFA faecalis
                        (Streptococcus faecalis)] AA
                        align

```

Score = 575 bits (1481), Expect = e-163
Identities = 288/400 (72%), Positives = 328/400 (82%), Gaps = 6/400 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MAKEKF+R+ HVNIGTIGHV HGKTTL+AAI+ VLS G E + YD+IDNAP+EKERG
Sbjct: 1  MAKEKFDRSKSHVNIGTIGHVDHGKTTLTAATVLSKHGGGEAQSYDSIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
        ITI TSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 61  ITINTSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LLSR VGVP+IVVFINK                      S Y+FGDD P++AGSAL+ALE
Sbjct: 121  LLSRNVGVPIIVFLNKMMDVDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVVTGRIERG 240
        ++      + EK+L+LMA VD YIPTPERD+K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  GDES-----YEEKILELMAAVDEYIPTPERDTPKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGIR-ATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
        V+VGDEVEIVGI+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E++ERG VL
Sbjct: 236  EVRVGDEVEIVGIKDETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIERGQVLA 295

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Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPPQFYVRTTDDVTGSITLPEGVEMVMPG 359
 KP +ITPH KP+ E+YVLSKEEGGRHTPFFFTNYRPPQFY RRTDVTG + LPEG EMVMPG
 Sbjct: 296 KPATITPHTKFKAEVYVLSKEEGGRHTPFFFTNYRPPQFYRRTTDDVTGTVVVELPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV + VELI P+A+E GT+F+IREGGRTVG+GVV+ I++
 Sbjct: 356 DNVAMDVELIHPIAIEDGTRFSIREGGRTVGSGVVTEIVK 395

tr Q5NID9 Elongation factor Tu (EF-Tu) [tufA] [Francisella 394
 Q5NID9_FRATT tularensis (subsp. AA
 tularensis)] align

Score = 574 bits (1480), Expect = e-162
 Identities = 281/399 (70%); Positives = 328/399 (81%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF R+ PHVN+GTIGHV HGKTTL+AAI+ V++ K + +D ID+AP+EK RG
 Sbjct: 1 MAKEKFERSKPHVNVGTIGHVDHGKTTLTAAITKVMAEKNGGMARKFDEIDSAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120
 ITI TSH+EYE+ RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI
 Sbjct: 61 ITINTSHVEYESPNRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP IVVFLNK YEFPGDDT++ GSALKA+E
 Sbjct: 121 LLSRQVGVPKIVVFLNKCDMVDDEELLELVEMEVRELLDQYEFPGDDTPVIMGSALRAIE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVTGRIERG 240
 +A + EK+++L+ +D YIP PERDTEK F++P+EDVESI+GRGTVVTGRIERG
 Sbjct: 181 GDEA-----YVEKIVELVQAMDDYIPAPERDTEKPFILPIEDVFSISGRGTVVTGRIERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 VV +GDEVE+VGIR TQKTTVTGVEMFRK L++GEASDNVG+L+RG K+++VERG VLCK
 Sbjct: 236 VVNIGDEVEVVGIRPTQKTTVTGVEMFRKLLDRGEAGDNVGILVRGLKRDDVERGQVLCK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
 PGSI PH KFE E+YVLSKEEGGRHTPFF YRPPQFY RRTD+TG++ LPEGVEMVMPGD
 Sbjct: 296 PGSIKPHTKFEAEVYVLSKEEGGRHTPFFKGYRPPQFYRRTTDDITGAVELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NVK+T+ LI+P+A++ G +FAIREGGRTVGAGVV+ IIE
 Sbjct: 356 NVKMTITLINPIAMDEGLRFAIREGGRTVGAGVVAKIIE 394

sp Q8XGZ0 Elongation factor Tu (EF-Tu) [tufA] [Ralstonia 396
 EFTU_RALSO solanacearum AA
 (Pseudomonas solanacearum)] align

Score = 573 bits (1477), Expect = e-162
 Identities = 289/400 (72%); Positives = 327/400 (81%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K E K YD ID AP+EK RG
 Sbjct: 1 MAKEKFERTKPHVNVGTIGHVDHGKTTLTAAIATVLSKFGGEAKKYDEIDAAPEEKARG 60

```

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI T+HIEYET RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 61 ITINTAHIEYETANRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+I+VFLNK S Y+FPGDDTPI+ GSA ALE
Sbjct: 121 LLARQVGVPYIIVFLNKCDMVDDAELELVEMEVRELLSKYDFPGDDTPIIKGSAKLALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AE-VDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIER 239
      G+ GE GE + +A+ +DSYIPTPER + TFLMPVEDVFSI+GRGT VVTGRIER
Sbjct: 181 ----GDKGELGEVAIMNLADALDSYIPTPERAVDGTFLMPVEDVFSISGRGT VVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      G++KVG+E+EI VGI+ATQKTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VLC
Sbjct: 237 GIIKVGEEIEIVGIKATQKTTCTGVEMFRKLLDQGGAGDNVGILLRGTKREDVERGQVLC 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYPQFYVRTT DVTGSITLPEGVEMVMPG 359
      KPGSI PH F E+Y+LSK+EGGRHTFFF NYRPQFY RTT DVTGSI LP+ EMVMPG
Sbjct: 297 KPGSIKPHHTFTGEVYILSKDEGGRHTPFFNNYRPQFYFRTT DVTGSIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ IIE
Sbjct: 357 DNVSITVKLIAPIAMEEGLRFAIREGGRTVGAGVVAKIIE 396

```

tr Q7M7F1 Translation elongation factor Tu (EC 3.6.1.48) [tufA] 396 AA
 Q7M7F1_CHRVO [Chromobacterium violaceum]
 align

Score = 573 bits (1477), Expect = e-162

Identities = 286/399 (71%), Positives = 329/399 (81%), Gaps = 5/399 (1%)

```

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      MAKEKE RT PHVN+GTIGHV HGKTTL+AAI+ +LS K E KDY ID+AP+EK RG
Sbjct: 1 MAKEKFERTKPHVNVGTIGHVDHGKTTLTAAITILSKKFGGEAKDYSQIDSAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI T+H+IEYETETRHYAHVDCPGHADYVENMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 61 ITINTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+I+V+LNK S+Y+FPGDDTPIV GSA ALE
Sbjct: 121 LLSRQVGVPYIIVYLNKADLVDDAELELVEMEVRLDLSYDFPGDDTPIVTGSARLALE 180

Query: 181 EAKAGNVGEWGE-KVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIER 239
      G+ E GE + +L +DSYIPTPER +K FL+P+EIVFSI+GRGT VVTGR+ER
Sbjct: 181 ----GDQSEMGEPSIFRLADALDSYIPTPERAIDKPFLLPIEDVFSISGRGT VVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      G+VKG+E+EI V++ T KTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VL
Sbjct: 237 GIVKVGEEIEIVGLKDTVKTCTGVEMFRKLLDQGGAGDNVGVLLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYPQFYVRTT DVTGSITLPEGVEMVMPG 359
      KPG+ITPH KFE +YVLSK+EGGRHTFFF NYRPQFY RTT DVTG+I+L EGVEMVMPG
Sbjct: 297 KPGTITPHTKFEASVYVLSKDEGGRHTPFFANYRPQFYFRTT DVTGAISLAEGVEMVMPG 356

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Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
 DNV+I VELI+P+A+E G +FAIREGGRTVGAGV+ II
 Sbjct: 357 DNVEIKVELIAPIAIEEGLRFAIREGGRTVGAGVAKII 395

sp Q50306 Elongation factor Tu (EF-Tu) [tuf] [Bacillus 395
 EFTU_BACST *stearothermophilus*] AA
align

Score = 571 bits (1472), Expect = e-162
 Identities = 283/400 (70%), Positives = 327/400 (81%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KF RT PHVNIGTIGHV HGKTTL+AAI+ VL+ +G AE K YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERTKPHVNIGTIGHVDHGKTTLTAAITTVLAKQGKAEAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI+T+H+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
 Sbjct: 61 ITISTAHVEYETEARHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVFLNK S Y+FEED+ P++ GSAL+ALE
 Sbjct: 121 LLSRQVGVPYIVVFLNKCDMVDDEELLELVEMEVRDLLSEYDFPGDEVPVIGKSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVTGRIERG 240
 +W EK+++LM VD YITP+R+ +K F+MP+EDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GDPKWEKIIELMNAVDEYIPTQREVDPKPFMPPIEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQK-TTVTGVMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 +KVGQ VEL+G+ K TTVTGVMFRK L++ EAGDN+G LRK ++EVERG VL
 Sbjct: 236 TLKVGDPVEIIGLSDEPKATTVTGVEMFRKLLDQAEAGDNIGALLRGVSRDEVERGQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPPQFYVRTTDDVTGSITLPEGVEMVMPG 359
 KPGSITPH KF+ ++YVL+KEEGGRHTFFF+NYRPPQFY RTTDDVTG ITLPEGVEMVMPG
 Sbjct: 296 KPGSITPHTKFKAQVYVLTKEEGGRHTPFFSNYRPPQFYFRTTDDVTGIITLPEGVEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV++TVELI+P+A+E GTKF+IKEGGRTVGAG VS IIE
 Sbjct: 356 DNVENTVELIAPIAIEEGTKFSIREGGRTVGAGSVSEIIE 395

tr Q5L3Z9 Translation elongation factor Tu (EF-Tu) [tufA] 395
 Q5L3Z9_GEOKA [Geobacillus
 kaustophilus] AA
align

Score = 570 bits (1470), Expect = e-161
 Identities = 282/400 (70%), Positives = 327/400 (81%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KF RT PHVNIGTIGHV HGKTTL+AAI+ VL+ +G AE K YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERTKPHVNIGTIGHVDHGKTTLTAAITTVLAKQGKAEAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI

Sbjct: 61 ITISTAHVEYETDARHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVFLNK S Y+FPGD+ P++ GSAL+ALE

Sbjct: 121 LLSRQVGVPPIVFLNKCDMVDDEELLELVEMEVRLDSEYDFPGDEVPIKGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
 +W EK+++LM VD YIPTP+R+ +K F+MP+EDVFSI GRGTV TGR+ERG

Sbjct: 181 -----GDPQWEEKIIELMNAVDEYIPTPQREVDPKFMPIEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQK-TTGTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 +KVGQ VEL+G+ K TTGTGVEMFRK L++ EAGDN+G LLRG ++EVERG VL

Sbjct: 236 TLKVGDPVEIIGLSDEPKTTTGTGVEMFRKLLDQAEAGDNIGALLRGVSRDEVERGQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPG 359
 KPGSITPH KF+ ++YVL+KEEGGRHTPFF+NYRPQFY RTTDTG SIITLPEGVEMVMPG

Sbjct: 296 KPGSITPHTKFKAQVYVLTKEEGGRHTPFFSNYRPQFYFRTTDTGTIITLPEGVEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV++TVELI+P+A+E GTKF+IREGGRTVGAG VS IIE

Sbjct: 356 DNVENTVELIAPIAIEEGTKFSIREGGRTVGAGSVSEIIE 395

tr Q5P334 Elongation factor Tu [tufB] [Azoarcus sp. (strain EbN1)] 396 AA
 Q5P334_AZOSE align

Score = 569 bits (1466), Expect = e-161
 Identities = 286/400 (71%), Positives = 326/400 (81%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ +LS K E K YD ID AP+EK RG

Sbjct: 1 MAKGKFERTKPHVNVGTIGHVDHGKTTLTAAITILSKKFGGEAKAYDQIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI T+H+EYET RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI

Sbjct: 61 ITINTAHVEYETANRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VFLNK S Y+FPGD+ PI+ GSAL+ALE

Sbjct: 121 LLARQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSKYDFPGDDVPIIKGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AE-VDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239
 G+ +GE + +AE +DSYIPTPER ++ EL+P+EDVESI+GRGTVVTGR+ER

Sbjct: 181 ----GDQSDIGEPAIFRLAEALDSYIPTPERAIDRPFLPIEDVFSISGRGTVVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTGTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+VVKVG+EVEIVGI+AE KTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VLC

Sbjct: 237 GIVKVGEEVEIVGIKATVKTCTGVEMFRKLLDQGGAGDNVGVLLRGTKREDVERGQVLC 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPG 359
 KPGSI PH F E+YVLSKEEGGRHTPFF NYRPQFY RTTDTGSI LPEG EMVMPG

Sbjct: 297 KPGSIKPHTHFTGEVYVLSKEEGGRHTPFFNNYRPQFYFRTTDTGSIELPEGTEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV ITV+L++P+A+E G +FAIREGGRTVGAGV+ IIE

Sbjct: 357 DNVSITVKLMAPIAMEEGLRFAIREGGRTVGAGVVAKIIIE 396

sp Q8R7T8 Elongation factor Tu-B (EF-Tu-B) [tufB] 400
 EFTU2_THETN [Thermoanaerobacter 400
 tengcongensis] align

Score = 568 bits (1464), Expect = e-161
 Identities = 284/400 (71%), Positives = 323/400 (80%), Gaps = 1/400 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK+KF RT PHVN+GTIGHV HGKTTL+AAI+ +LS GLA+ K YD ID AP+EK RG
 Sbjct: 1 MAKQKFERTKPHVNVGTIGHVDHGKTTTLTAAILLILSKAGLAQAKGYDEIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI T+H+EYET RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
 Sbjct: 61 ITINTTHVEYETAKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+IVVFLNK + YEFPGD+TPIV GSAL+ALE
 Sbjct: 121 LLARQVGVPYIVVFLNKADMVDDPELIELVEMEVDRLLNQYEFPGDETPIVVGSALEKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
 +W K+ +LM VD YIPTPERD +K FLMPVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 CGCGKRECQWCGKIWELMDVVDEYIPTPERDIDKPFMLPVEDVFSITGRGTVATGRVERG 240

Query: 241 VVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 VVKVGDEVEI+G+ ++KT VTGVEMFRK L++ +AGEN+GVLLRG +K+EVERG VL
 Sbjct: 241 KVKVGDEVEIIGLTTESRKTVVTGVEMFRKTLDEAQAGDNIGVLLRGIQKDEVERGQVLA 300

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIPLPEGVEMVMPG 359
 KPG+I PH KFE ++YVL+KEEGGRHTPEFF YRPQFY RTTDTGTG+I LPEGVEMVMPG
 Sbjct: 301 KPGTIKPHTKFEAQVYVLTKEEGGRHTPFFNGYRPFYFRTTDTGTIQLPEGVEMVMPG 360

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 D+V + VELI+P+A+E G KFAIREGGRTVGAGVVS IIE
 Sbjct: 361 DHVTLRVELITPIAMEEGLKFAIREGGRTVGAGVVSIIIE 400

sp Q8R603 Elongation factor Tu (EF-Tu) [tuf] [Fusobacterium 394
 EFTU_FUSNN nucleatum (subsp. 400
 nucleatum)] align

Score = 568 bits (1463), Expect = e-160
 Identities = 280/397 (70%), Positives = 324/397 (81%), Gaps = 5/397 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEK+ R+ PHVNIGTIGHV HGKTT +AAIS VLS KG A D+D ID AP+EKERG
 Sbjct: 1 MAKEKYNRSKPHVNIGTIGHVDHGKTTTAAISKVLSKDWASKVDFDQIDAAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI T+H+IEYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
 Sbjct: 61 ITINTAHIEYETEKRYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180

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      LLSRQVGVP+IVV+LNK                      + Y FPGDD P++ GS+L AL
Sbjct: 121 LLSRQVGVPYIVVYLNKSDMVEDEELLELVEMEVRELLTEYGFPGDDIPVIRGSSLGALN 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      +      +W EK+L+LM VD+YIETPER ++ FLMP+EDVF+I GRGTVVTGR+ERG
Sbjct: 181 GEE-----KWVEKILELMEAVDNYIPTPERAVDQPFILMPIEDVFTITGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      V+KVG+E+EI VGI+ T KTF TGVEMFRK L++G+AGDN+GVLLRGTKKEEVERG VL K
Sbjct: 236 VIKVGEEIEIVGIKPTTKTTCTGVEMFRKLLDQGGAGDNIGVLLRGTKKEEVERGQVLAK 295

Query: 301 PGSITPHKKFEEIEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPGD 360
      PGSI PH F+ E+YVL+K+EGGRHTPEFT YRPQFY RTTD+TG++TLP+GVEMVMPGD
Sbjct: 296 PGSIHPHTNFKGEVYVLTKEGGGRHTPFFTGYRPQFYFRTTDTITGAVTLPDGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
      N+ +TVELI P+A+E G +FAIREGGRTV +GVVS I
Sbjct: 356 NITMTVELIHPIAMEQGLRFAIREGGRTVASGVVSEI 392

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tr Q63PZ6 **Elongation factor Tu [tufA1] [Burkholderia pseudomallei 396 AA**
Q63PZ6_BURPS **(Pseudomonas pseudomallei)]**

align

Score = 568 bits (1463), Expect = e-160
Identities = 287/400 (71%), Positives = 325/400 (80%), Gaps = 5/400 (1%)

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Query: 1  MAKEKFNRNTNPVNIHTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAKEKF RT PHVN+GTIGHV HOKTTL+AAI+ VLS K E K YD ID AP+EK RG
Sbjct: 1  MAKEKFERTKPHVNVGTIGHVDHGKTTTLTAAIATVLSAKFGGEAKKYDEIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQOTREHI 120
      ITI T+HIEYET RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQOTREHI
Sbjct: 61 ITINTAHIEYETANRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQOTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+I+VFLNK                      S Y+FPGDDEPTI+ GSA ALR
Sbjct: 121 LLARQVGVPYIIVFLNKCDMVDDAEELLELVEMEVRELLSKYDFPGDDTPIIKGSAKLAL 180

Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239
      G+ GE GE + +A+ +D+YIETPER + FILMPVEDVFSI+GRGTVVTGR+ER
Sbjct: 181 ----GDKGELGEVAIMNLADALDYIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      GV+KVG+E+EI VGI+AE KTF TGVEMFRK L++G+AGDNV+LLRGTK+E+VERG VL
Sbjct: 237 GVIKVGEEIEIVGIKATAKTTCTGVEMFRKLLDQGGAGDNVGIILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPG 359
      KPGSITPH F E+YVLSK+EGGRHTPEFT NYRPQFY RTTDVTGSI LP+ EMVMPG
Sbjct: 297 KPGSITPHHTFAEVYVLSKDEGGGRHTPFNNYRPQFYFRTTDTGSIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNV ITV+LL+P+A+E G +FAIREGGRTVGAGV+ IIE
Sbjct: 357 DNVSITVKLIAPAMEEGLRFAIREGGRTVGAGVVAKIIE 396

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tr Q62GK3 Translation elongation factor Tu [tuf-1] [Burkholderia 396
 Q62GK3_BURMA mallei AA
 (Pseudomonas mallei)] align

Score = 568 bits (1463), Expect = e-160
 Identities = 287/400 (71%), Positives = 325/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAKEKF RT PHVN+GTIGHV HOKTEL+AAI+ VLS K E K YD ID AP+EK RG
 Sbjct: 1 MAKEKFERTKPHVNVGTIGHVDHGKTTLTAAIATVLSAKFGGEAKKYDEIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGPMPTREHI 120
 ITI T+HIEYET RHYAHVDCPGHADVKNMITGAAQMDGAILV SAADGPMPTREHI
 Sbjct: 61 ITINTAHIEYETANRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGPMPTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VFLNK S Y+FPGDDTPI+ GSA ALE
 Sbjct: 121 LLARQVGVPYIIIVFLNKCDMVDDAELELVEMEVRELLSKYDFPGDDTPIIKGSAKLAL 180

Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIER 239
 G+ GE GE + +A+ +D+YIPTPER + FLMPVEDVFSI+GRGTVVTGR+ER
 Sbjct: 181 ----GDKGELGEVAIMNLADALDTYIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 GV+KVG+E+EIIVGL+AT KPT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL
 Sbjct: 237 GVIKVGEEIEIVGIKATAKTTCTGVEMFRKLLDQGGAGDNVGILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSIPLPEGVEMVMPG 359
 KPGSITPH F E+YVLSK+EGGRHTPEE NYRPQFY RTTDTGSI LP+ EMVMPG
 Sbjct: 297 KPGSITPHTHFTAEVYVLSKDEGGRHTPFFNNYRPQFYFRTTDTGSIPLPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ IIE
 Sbjct: 357 DNVSITVKLIAPIAMEEGLRFAIREGGRTVGAGVVAKIIE 396

sp P42481 Elongation factor Tu (EF-Tu) [tuf] [Thiobacillus cuprinus] 396 AA
 EFTU_THICU align

Score = 567 bits (1462), Expect = e-160
 Identities = 285/400 (71%), Positives = 324/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KF RT PHVN+GTIGHV HOKTEL+AAI+ VLS K E K YD ID AP+EK RG
 Sbjct: 1 MAKSKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLSSKFGGEAKAYDQIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGPMPTREHI 120
 ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGPMPTREHI
 Sbjct: 61 ITINTAHVEYETANRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGPMPTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VFLNK S Y+FPGDDTPI+ GSA ALE
 Sbjct: 121 LLARQVGVPYIIIVFLNKCDMVDDAELELVEMEVRELLSKYDFPGDDTPIIKGSAKLAL 180

Query: 181 EAKAGNVGEWGE-KVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIER 239
 G+ GE GE +IKL +D+YIPTPER + FLMPVEDVFSI+GRGTVVTGR+ER

Sbjct: 181 ----GDKGELGEGAILKLAELDTYIPTPERAVDGAFLMPVEDVFSISGRGTVVTRGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
G++KVG+E+EVG++ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+EEVERG VLC

Sbjct: 237 GIIKVGEEIEIVGLKPTLKTTCTGVEMFRKLLDQGGAGDNVGILLRGTKREEVERGQVLC 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGTSITLPEGVEMVMPG 359
KPGSI PH F E+YVLSK+EGGRHTPFF NYRPQFY RTTDTG+I LP+ EMVMPG

Sbjct: 297 KPGSIKPHHTFAEVYVLSKDEGGGRHTPFFNNYRPQFYFRTTDTGAIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ IIE

Sbjct: 357 DNVSITVKLIAPIAMEEGLRFAIREGGRTVGAGVVAKIIE 396

sp P48864 Elongation factor Tu (EF-Tu) [tuf] [Neisseria gonorrhoeae] 394 AA
EFTU_NEIGO

align

Score = 567 bits (1462), Expect = e-160

Identities = 280/398 (70%), Positives = 327/398 (81%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
MAKEKF R+ PHVN+GTIGHV HGKTTL+AA++ +L+ K K YD IDNAP+EK RG

Sbjct: 1 MAKEKFERSKPHVNVGTIGHVDHGKTTLTAAITLAKKFGGAAYDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
ITI TSH+EYETETRHYAHVDCPGHADVKNMITGAAQMDGAILV SAADGMPQTREHI

Sbjct: 61 ITINTSHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQGVGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
LL+RQGVGV+I+VE+NK S+Y+FPGDD PIV GSAL+ALE

Sbjct: 121 LLARQGVGPYIIVFMNKCDDVDAELFQLVEMEIRDLLSSYDFPGDDCPIVQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
A + EK+ +L +D YIPTER +K EL+P+EDVFSI+GRGTVVTR+ERG

Sbjct: 181 GDA-----YEEKIFELATALDRYIPTPERAVDKPFLLPIDVFSISGRGTVVTRGRVER 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
++ VGDE+ELVG++ TQKTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL K

Sbjct: 236 IIVGVDEIEIVGLKETQKTTCTGVEMFRKLLDEGQAGDNVGVLLRGTKREDVERGQVLAK 295

Query: 301 PGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGTSITLPEGVEMVMPGD 360
G+ITPH KF+ E+YVLSKEEGG HTFFF NYRPQFY RTTDTG+ITL +GVEMVMPG+

Sbjct: 296 RGTITPHTKFAEVYVLSKEEGGPHTPFFANYRPQFYFRTTDTGTITLEKGVEMVMPGE 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 398
NV ITVELI+P+A+E G +FAIREGGRTVGAGVVS++I

Sbjct: 356 NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVVSNI 393

sp Q8R7V2 Elongation factor Tu-A (EF-Tu-A) [tufA]
EFTU1_THETN [Thermoanaerobacter
tengcongensis]

400

AA

align

Score = 567 bits (1462), Expect = e-160

Identities = 283/400 (70%), Positives = 323/400 (80%), Gaps = 1/400 (0%)

```
Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK+KF RT PHVN+GTIGHV HGKTTL+AAI+ +LS GLA+ K YD ID AP+EK RG
Sbjct: 1  MAKQKFERTKPHVNVGTIGHVDHGKTTLTAAITLILSKAGLAQAKGYDEIDKAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120
      ITI T+H+EYET RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI
Sbjct: 61  ITINTTHVEYETAKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+IVVFLNK + YEFPGDDTPIV GSAL+ALE
Sbjct: 121  LLARQVGVPYIVVFLNKADMVDDPELIELVEMEVRLDNLNQEYFPDDTPIVVSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVVGRIERG 240
      +W K+ +LM VD YITPERD +K FIMPVEDVF+I GRGTV TGR+ERG
Sbjct: 181  CGCGKRECQWCGKIWELMDVDEYIPTPERDIDKPFMLPVEDVFTITGRGTVATGRVERG 240

Query: 241  VVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLC 299
      VVKVGDEVEL+G+ ++KT VTGVEMFRK L++ +AGDN+GVLEKRG +++EVERG VL
Sbjct: 241  KVKVGDEVEIIGLTTESRKTVVTGVEMFRKTLDEAQAGDNIGVLLRGIQRDEVERGQVLA 300

Query: 300  KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVVRTTDTGSIITLPEGVEMVMPG 359
      KPG+I PH KFE ++YVL+KEEGGRHTPFF YRPQFY RTTDTVG+I LPEGVEMVMPG
Sbjct: 301  KPGTIKPHTKFEAQVYVLTKEEGGRHTPFFNGYRPFYFRTTDTGTIQLPEGVEMVMPG 360

Query: 360  DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      D+V + VELI+P+A+E G KFAIREGGRTVGAGVVS IIE
Sbjct: 361  DHVTLRVELITPIAMEEGLKFAIREGGRTVGAGVVSNIIE 400
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tr Q83ES6      Translation elongation factor Tu [tuf-2] [Coxiella      397
    Q83ES6_COXBU burnetii]      AA
                                align
```

Score = 567 bits (1462), Expect = e-160

Identities = 281/400 (70%), Positives = 333/400 (83%), Gaps = 4/400 (1%)

```
Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      M+KEKF R PHVN+GTIGHV HGKTTL+AA++ VLS K E K +D IDNAP+E+ RG
Sbjct: 1  MSKEKFVREKPHVNVGTIGHVDHGKTTLTAAITKVLSEKYGGEKKAQFDQIDNAPEERARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120
      ITIATSH+EY+++ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI
Sbjct: 61  ITIATSHVEYQSDKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      +L++QVGVP+IVV+LNK +Y+FPGD+TPT+ GSAL+ALE
Sbjct: 121  VLAKQVGVPNIVVYLNKADMVDDKELLELVEMEVRLDNLNSYDFPGDETPIIVGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVVGRIERG 240
      K+ VGE ++KL+ +D+Y P EER +K FLMP+EDVEST+GRGTVVVTGR+ERG
Sbjct: 181  GDKS-EVGE--PSIIKLVTMDTYFPQPERAIDKPFMLPIEDVFSISGRGTVVVTGRVERG 237

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300
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      ++KVGDE+EIVGI+ T KTF TGVMFRK L++G+AGDNVG+LLRGTG+EEVERG VL K
Sbjct: 238 IIKVGDEIEIVGIKDTTKTTCTGVEMFRKLLDEGQAGDNVIGILLRGTGKREEVERGQVLAK 297

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGS-ITLPEGVEMVMPG 359
      PGSITPHKKFE EIVVLSKEEGGRHTPF YRPQFY RTTDTG ++LPEG+EMVMPG
Sbjct: 298 PGSITPHKKFEAEIYVLSKEEGGRHTPFQGYRPFYFRTTDTVGTQLLSLPEGIEMVMPG 357

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNVK+TVELI+EVA++ G +FA+REGGRTVGAGVV+ IIE
Sbjct: 358 DNVKVTVELIAPVAMDEGLRFAVREGGRTVGAGVVTKIIE 397

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tr Q7P364      Protein translation elongation factor Tu (EF-TU)      394
Q7P364_FUSNV [FNV2036]      AA
      [Fusobacterium nucleatum subsp. vincentii ATCC 49256]      align

```

Score = 567 bits (1462), Expect = e-160
 Identities = 279/399 (69%), Positives = 326/399 (80%), Gaps = 5/399 (1%)

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Query: 1  MAKEKFNRNTNPVHNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAKEK+ R+ PNVNIGTIGHV HOKTT +AAIS VLS KGLA D+D ID AP+EKERG
Sbjct: 1  MAKEKYERSKPHVHNIGTIGHVDHGKTTTAAISKVLSKGLASKVDQIDAAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI T+HIEYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 61  ITINTAHIEYETANRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121  LLSRQVGVPVHIVVFLNXXXXXXXXXXXXXXXXXXXXXAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+I+V+LNK + Y FPGD+ P++ GS+L AL
Sbjct: 121  LLSRQVGVPYIIIVYLNKADMVDDEELLELVEMEVRELLTEYGFPGDEIPVIRGSSLGALN 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
      + +W EK++LM VDSYIPTPER ++ FLMP+EDVE+I GRGTVVTGR+ERG
Sbjct: 181  GEE-----KWIEKIMELMDAVDSYIPTPERAIDQFLMPIEDVFTITGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTGKKEEVERGMVLCK 300
      V+KVG+E+EIVGI+ T KTF TGVMFRK L++G+AGDN+GVLLRGTGKKEEVERG VL K
Sbjct: 236  VIKVGEEIEIVGIKPTTKTTCTGVEMFRKLLDQGGAGDNIGVLLRGTGKKEEVERGQVLAK 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
      PGSI PH F+ E+YVLD+N+EGGRHTPFET YRPQFY RTTD+TG++TLP+GVEMVMPGD
Sbjct: 296  PGSIHPTNFKGEVYVLTKEGGRHTPFFTGYRPFYFRTTDTITGAVTLPDGVEMVMPGD 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      N+ +TVELI P+A+E G +FAIREGGRTV +GVVS II+
Sbjct: 356  NITMTVELIHPIAMEQGLRFAIREGGRTVASGVVSEIIK 394

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tr Q7TTF9      Elongation factor tu, EF-Tu [tufA] [Haemophilus ducreyi] 394 AA
Q7TTF9_HAEDU
      align

```

Score = 567 bits (1461), Expect = e-160
 Identities = 279/399 (69%), Positives = 323/399 (80%), Gaps = 5/399 (1%)


```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        M+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG
Sbjct: 1  MSKEKFERTKPHVNVGTIGHVDHGKTTTLTAAITTVLAKHFGGAARAFDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
        ITI TSH+EY+TETRHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61  ITINTSHVEYDTETRHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LL RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+AL
Sbjct: 121  LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRSALQALN 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
        V EW EK+++L +DSYIP PER +K FL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 181  -----GVPEWEEKIIE LAQHLD SYIPEPERAIDKPFLLPIEDVFSISGRGT VVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        ++K G+EVEIVGI+ T KTTVTGVEMFRK L++G AG+NVG LLRGTK+EE+ERG VL K
Sbjct: 236  IIKSGEEVEIVGIKETT KTTVTGVEMFRKLLDEGRAGENVGALLRGTKREEIERGQVLAK 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPF FTYRQFYVRTT DVTGSITLPEGVEMVMPGD 360
        PG+ITPH FE E+YVLSKEEGGRHTPF F YRQFY RTT DVTG+I LPEGVEMVMPGD
Sbjct: 296  PGTITPHTDFESEVYVLSKEEGGRHTPF FFKGYRQFYRTT DVTGTIELPEGVEMVMPGD 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTV GAGVVSNIIE 399
        N+K+TV LI P+A++ G +FAIREGGRTV GAGVV+ LI+
Sbjct: 356  NIKMTVSLIHPAMDEGLRFAIREGGRTV GAGVWAKIIK 394

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sp Q99QMO Elongation factor Tu (EF-Tu) [tufA] [Caulobacter 396
   EFTU_CAUCR crescentus] AA
                                align

```

Score = 566 bits (1460), Expect = e-160
Identities = 285/399 (71%), Positives = 323/399 (80%), Gaps = 3/399 (0%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MAKEKF RT PH NIGTIGHV HGKTTL+AAI+ L+ G A K YD ID AP+EK RG
Sbjct: 1  MAKEKFERTKPHCNIGTIGHVDHGKTTTLTAAITMTLAKSGGATAKKYDEIDAAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
        ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 61  ITINTAHVEYETANRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LL+RQVGVP +VVF+NK S+Y+FPGDD PI GSAL A+E
Sbjct: 121  LLARQVGVPALVVF MNKVDMDDEELLELVEMEVRELLSSYQFPGDDIPITKGSALAAVE 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
        + +GE EK+L+LMA VD+YIP PER + FIMPVEDVFSI+GRGT VVTGR+ERG
Sbjct: 181  -GRDPQIGE--EKILELMASVDAYIPQPERPVDMPFLMPVEDVFSISGRGT VVTGRVERG 237

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        +VVG+EVEIVGIR QKTT TGEMFRK L++G+AGDNVGVLLRGTK+E+VERG VLCK
Sbjct: 238  IVKVGEEVEIVGIRPVQKTTCTGVEMFRKLLDQGGAGDNVGVLLRGTKREDVERGQVLCK 297

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Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
 PGSTTPH KF E Y+L+KEEGGRHTPFFFTNYRPQFY RTTDDVTG I L EGVEN+MPGD
 Sbjct: 298 PGSITPHTKFVAEAYILTKEEGGRHTPFFFTNYRPQFYRTTDDVTGIIKLREGVEMIMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 N ++ VELI+P+A+E +FAIREGGRTVGAGVV+ I+E
 Sbjct: 358 NAELDVELITPIAMEEKLRFIREGGRTVGAGVVAKIVE 396

sp Q8Y422 Elongation factor Tu (EF-Tu) [tuf] [Listeria 395
 EFTU_LISMO monocytogenes] AA
align

Score = 566 bits (1459), Expect = e-160
 Identities = 277/398 (69%), Positives = 325/398 (81%), Gaps = 6/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF+R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ KG A+ + YD ID AP+E+ERG
 Sbjct: 1 MAKEKFDRSKPHVNIGTIGHVDHGKTTLTAAITTVLAKKGYADAQAYDQIDGAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI+T+H+EY+T++RHVAVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI
 Sbjct: 61 ITISTAHVEYQTDsrHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPVPHIVVFLNXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVP+HK + YEFPGDD P++ GSAL+AL+
 Sbjct: 121 LLSRQVGVPYIVVFMNKCMDVDEELLELVEMEIRDLLTEYEFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVTGRIERG 240
 +W K+ +LM VDSYIPTPERDT+E F+MPVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GEADWEAKIDELMEAVDSYIPTPERDTEKTFMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 VVKVGDEVE++GI ++K VTGVEMFRK L+ EAGDN+G LLRG +E+++RG VL
 Sbjct: 236 QVKVGDEVEVIGIEEESKKVVVTGVEMFRKLLDYAAGDNIGALLRGVAREDIQRQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPG 359
 KPGSITPH F+ E YVL+KEEGGRHTPFF NYRPQFY RTTDDVTG +TLPEG EMVMPG
 Sbjct: 296 KPGSITPHTNFKAETYVLTKEEGGRHTPFFFTNYRPQFYRTTDDVTGIVTLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
 DN+++ VELI+P+A+E GKTF+IREGGRTVGAGVVSNI
 Sbjct: 356 DNIELAVELIPIAIEDGTFKSIREGGRTVGAGVVSNI 393

sp Q71WB9 Elongation factor Tu (EF-Tu) [tuf] [Listeria monocytogenes 395 AA
 EFTU_LISMF (serotype 4b / strain F2365)]
align

Score = 566 bits (1459), Expect = e-160
 Identities = 277/398 (69%), Positives = 325/398 (81%), Gaps = 6/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF+R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ KG A+ + YD ID AP+E+ERG
 Sbjct: 1 MAKEKFDRSKPHVNIGTIGHVDHGKTTLTAAITTVLAKKGYADAQAYDQIDGAPEERERG 60

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Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
          ITI+T+H+EY+T++RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI
Sbjct: 61  ITISTAHVEYQTDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
          LLSRQVGVP+IVVF+NK                      + YEFPGDD P++ GSAL+AL+
Sbjct: 121  LLSRQVGVPYIVVFMNKCMDVDEELLELVEMEIRDLLTEYEFPGDDIPVIKGSALKALQ 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
          +W K+ +LM VDSYIPTPERDT+K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  -----GEADWEAKIDELMEAVDSYIPTPERDTPKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
          VVKVGDEVE++GI ++K VTGVEMFRK L+ EAGDN+G LRG +E+++RG VL
Sbjct: 236  QVKVGDEVEVIGIEEESKVVVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300  KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
          KPGSITPH F+ E YVL+KEEGGRHTFFF NYRPQFY RTTDTVG +TLPEG EMVMPG
Sbjct: 296  KPGSITPHTNFKAETYVLTKEEGGRHTPFFNNYRPQFYFRTTDTGIVTLPEGTEMVMPG 355

Query: 360  DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
          DN+++ VELL+P+A+E GTFK+IREGGRTVGAGVVSNI
Sbjct: 356  DNIELAVELIPIAIEDGTFKSIREGGRTVGAGVVSNI 393

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sp. Q927I6 **Elongation factor Tu (EF-Tu) [tuf] [Listeria innocua]** 395 AA
 EFTU_LISIN

align

Score = 566 bits (1459), Expect = e-160

Identities = 277/398 (69%), Positives = 324/398 (80%), Gaps = 6/398 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
          MAKEKF+R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ KG A+ + YD ID AP+E+ERG
Sbjct: 1  MAKEKFDRSKPHVNIGTIGHVDHGKTTLTAAITTVLAKKGFADAQAYDQIDGAPEERERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
          ITI+T+H+EY+T+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI
Sbjct: 61  ITISTAHVEYQTDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
          LLSRQVGVP+IVVF+NK                      + YEFPGDD P++ GSAL+AL+
Sbjct: 121  LLSRQVGVPYIVVFMNKCMDVDEELLELVEMEIRDLLTEYEFPGDDIPVIKGSALKALQ 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
          +W K+ +LM VDSYIPTPERDT+K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  -----GEADWEAKIDELMEAVDSYIPTPERDTPKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
          VVKVGDEVE++GI ++K VTGVEMFRK L+ EAGDN+G LRG +E+++RG VL
Sbjct: 236  QVKVGDEVEVIGIEEESKVVVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300  KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
          KPGSITPH F+ E YVL+KEEGGRHTFFF NYRPQFY RTTDTVG +TLPEG EMVMPG
Sbjct: 296  KPGSITPHTNFKAETYVLTKEEGGRHTPFFNNYRPQFYFRTTDTGIVTLPEGTEMVMPG 355

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Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
 DN+++ VELL+P+A+E GTKF+IREGGRTVGAGVVSNI
 Sbjct: 356 DNIELAVELIAPIAIEDGTKFSIREGGRTVGAGVVSNI 393

tr Q81ZS3 GTPases-translation elongation factors and sulfate 396
 Q81ZS3_NITEU adenylate AA
 transferase subunit 1 (EC 3.6.1.48) [tuf2] [Nitrosomonas align
 europaea]

Score = 565 bits (1457), Expect = e-160
 Identities = 280/399 (70%), Positives = 324/399 (81%), Gaps = 3/399 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KF R PHVN+GTIGHV HGKTTL+AAI+ +L+ K E K YD ID+AP+E+ RG
 Sbjct: 1 MAKSKFERVVKPHVNVGTIGHVDHGKTTLTAAITTLTKKFGGEAKSYDQIDSAPEERARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI TSH+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI
 Sbjct: 61 ITINTSHVEYETDKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVE+I+VF+NK S Y+FPGDDTPI+ GSAL+ALE
 Sbjct: 121 LLARQVGVPYIIVFMNKADMVDDAELELVEMEIRELLSNYDFPGDDTPIIIGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVTGRIERG 240
 K+ ++GE +LKL +DSYIP PER + F+MPVEDVFSI+GRGTVVTGR+ERG
 Sbjct: 181 GDKD-DIGE--AAILKLAEALDSYIPEPERAIDGAFIMPVEDVFSISGRGTVVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VVKVGDE+ELVG++ T KT TGVEMFRK L++G+AGDNVG+LLRGTK+EEVERG VL K
 Sbjct: 238 IVKVGDEIEIVGLKPTIKTVCTGVEMFRKLLDQGGAGDNVGILLRGTKREEVERGQVLAK 297

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTVTSITLPEGVEMVMPGD 360
 PGSI PH KF ELYVLSKEEGGRHTPFF YRPQFY RTTDTVTSI LP GVEMVMPGD
 Sbjct: 298 PGSILPHTKFTAIEIYVLSKEEGGRHTPFFAGYRPQFYFRTTDTVTSIELPAGVEMVMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 N+ +TV LI+P+A++ G +FAIREGGRTVGAGVV+ +IE
 Sbjct: 358 NISVTVNLIAPIAMDEGLRFAIREGGRTVGAGVVAKVIE 396

sp P57939 Elongation factor Tu-A (EF-Tu-A) [tufA] [Pasteurella 394
 EFTU1_PASMU multocida] AA
align

Score = 565 bits (1456), Expect = e-160
 Identities = 277/399 (69%), Positives = 323/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 M+KEKEF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG
 Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKHYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

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      ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL RQVGVP+I+VFLNK                      S Y+FPGDDTPI+ GSAL+AL
Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALQALN 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      V EW EK+L+L +D+YIP P+R ++ EL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 181 -----GVAEWEKILELANHLDTYIPEPQRAIDQPFLPIEDVFSISGRGT VVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +++ G+EVEIVGI+AT KTTVTGVEMFRK L++G AG+NVG LLRGTK+EE+ERG VL K
Sbjct: 236 IIRTGEEVEIVGIKATTKTTVTGVEMFRKLLDEGRAGENVGALLRGTKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTG SITLPEGVEMVMPGD 360
      PGSITPH FE E+YVLSKEEGGRHTPFF YRPQFY RTTDTG+I LPEGVEMVMPGD
Sbjct: 296 PGSITPHTDFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTTDTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      N+K+TV LI P+A++ G +FAIREGGRTVGAGVV+ II+
Sbjct: 356 NIKMTVSLIHPAMDQGLRFAIREGGRTVGAGVVAKIIE 394

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tr Q65QG6      TufB protein [tufB] [Mannheimia succiniciproducens] 394
Q65QG6_MANSMBEL55E] (strain AA
align

```

Score = 565 bits (1455), Expect = e-160

Identities = 276/399 (69%), Positives = 322/399 (80%), Gaps = 5/399 (1%)

```

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      M+KEKE RT PHVN+GTIGHV HGKTTLSAAI+ VLS + +D IDNAP+EK RG
Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLSKHYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL RQVGVP+I+VFLNK                      S Y+FPGDDTPI+ GSAL+ALE
Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      +W EK+L+L +D+YIP PER ++ EL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 181 -----GEAQWEEKILELANALDXYIPEPERAIDQPFLPIEDVFSISGRGT VVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +++ GDEVEIVGI+ T KTTVTGVEMFRK L++G AG+N+G LLRGTK+EE+ERG VL K
Sbjct: 236 IIRTGDEVEIVGIKETAKTTVTGVEMFRKLLDEGRAGENIGALLRGTKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTG SITLPEGVEMVMPGD 360
      PGSITPH FE E+YVLSKEEGGRHTPFF YRPQFY RTTDTG+I LPEGVEMVMPGD
Sbjct: 296 PGSITPHTDFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTTDTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

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N+K+TV LI P+A++ G +FAIREGGRTVGAGVV+ II+
 Sbjct: 356 NIKMTVSLIHPIAMDQGLRFAIREGGRTVGAGVVAKIHK 394

tr Q8L160 **Elongation factor Tu [tufA] [Myxococcus** 396 AA
Q8L160_MYXXA **xanthus]** align

Score = 565 bits (1455), Expect = e-160
 Identities = 283/400 (70%), Positives = 324/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF R PHVNIGTIGHV HGKT+L+AAI+ VL+ G A YD ID AP+E+ERG
 Sbjct: 1 MAKEKFNRTNPHVNIGTIGHVDHGKTSITAAITKVLAKTGGATFLAYDLIDKAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI+TSH+EY+T RHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI
 Sbjct: 61 ITISTSHVEYQTSNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+IVVFLNK YEFPDGD PI+ GSAL+ALE
 Sbjct: 121 LLARQVGVPPIVFLNKVMDLDDPELRELVEMEVDRLLKKEYPFGDDIPIPGSALKALE 180

Query: 181 EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVGTGRIER 239
 G+ + GE +LKLM VDSYIPTP+R T+K FLMPVEEDVFSI+GRGTV TGR+ER
 Sbjct: 181 ----GDTSDIGEPAILKLMEAVDSYIPTPQRATDKPFLMPVEDVFSISGRGTVATGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G++KVG+EVE+VG+R TQKT VTGVEMFRK L++G AGDN+G L+RG K+E++ERG VL
 Sbjct: 237 GIIKVGEEVEVGLRPTQKTTVTGVEMFRKLLDQGMAGDNIGALVRGLKREDMERGQVLA 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIPLPEGVEMVMPG 359
 KPGSITPH KF+ +IYVLSKEEGGRHTPFF YRPQFY RTTDTGGS+ LPE VEMVMPG
 Sbjct: 297 KPGSITPHTKFKAQIYVLSKEEGGRHTPFFKGYRPFYFRTTDTGSVKLPENVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+ I VELT+EVA+E +FA+REGGRTVGAGVV+ IIE
 Sbjct: 357 DNIAIEVELITPVAMEKELRFAVREGGRTVGAGVVAEIIIE 396

tr Q5FTY1 **Protein Translation Elongation Factor Tu (EF-TU)** 396
Q5FTY1_GLUOX **[GOX0382]** AA
[Gluconobacter oxydans (Gluconobacter suboxydans)] align

Score = 564 bits (1454), Expect = e-159
 Identities = 281/397 (70%), Positives = 326/397 (81%), Gaps = 3/397 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PH NIGTIGHV HGKT+L+AAI+ VL+ G A YD ID AP+E+ RG
 Sbjct: 1 MAKAKFERTKPHCNIGTIGHVDHGKTSITAAITKVLAKTGGATYSAYDQIDKAPEERARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI+T+R+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI
 Sbjct: 61 ITISTAHVEYETADRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180

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      LL+RQVGVP +VVFLENK                      S+Y+FPGDD PIV GSAL LE
Sbjct: 121 LLARQVGVPALVVFLNKVDQVDDPELLELVEMEVRLLSSYQFPGDDIPIVKGSALVTLE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      +   ++GE ++VL+LM +VD+YIP PER ++ FIMP+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181 DGDP-SIGE--DRVLELMTQVDAYIPQPERPVDRPFLMPIEDVFSISGRGTVVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      VV VGDEVEIVG++ T KTTVTGVEMFRK L++GEAGDN+G L+PGTK+E+VERG VL K
Sbjct: 238 VNVVGDEVEIVGLKDTVKTVTGVEMFRKLLDRGEAGDNIGALVRGTRKREDVERGQVLAK 297

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSITLPEGVEMVMPGD 360
      PGSITPHKKF+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTDTG +TLPEG EMVMPGD
Sbjct: 298 PGSITPHKKFKAAYILTKEEGGRHTPFFTNYRPQFYFRTTDTGVVTLPEGTEMVMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
      NV + VELI+P+A++ G +FAIREGGRTVGAGVVS+I
Sbjct: 358 NVAMDVELIAPIAMDEGLRFAIREGGRTVGAGVVSSI 394

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sp Q8ETY4      Elongation factor Tu (EF-Tu) [tuf] [Oceanobacillus      395
  EFTU_OCEIH iheyensis]      AA
                               align

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Score = 564 bits (1453), Expect = e-159
 Identities = 279/398 (70%), Positives = 322/398 (80%), Gaps = 6/398 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAKEK+K+ HVN+GT+GHV HGKTTL+AAI+ VL+ G E + YD ID AP+E+ERG
Sbjct: 1  MAKEKFDRSKSHVNVGTLGHVDHGKTTLTAAITTVLAKHGGGEARAYDQIDGAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LLSR VGVP VVFLENK                      + Y+FPGDD P++ GSAL+ALE
Sbjct: 121 LLSRNVGVPAPVVFLNKTDMDVDEELLELVEMEVRDLLTEYDFPGDDLPIVKGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      V E+ E++L+IMA VD YIPTPERD EK F+MPVEDVEST GRGTV TGR+ERG
Sbjct: 181 -----GVAEYEERILELMAAVDEYIPTPERDKEKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      VVKVGDEVET+G+ KTTVTGVEMFRK L+ EAGDN+G LLRG +E++ RG VL
Sbjct: 236 EVKVGDEVEIIGLAEDASKTTVTGVEMFRKLLDYAEAGDNIGALLRGVSREDINRGQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSITLPEGVEMVMPG 359
      KPGSITPH F+ E+YVLSKEEGGRHTPFFT+NYRPQFY RTTDTG I LPFG EMVMPG
Sbjct: 296 KPGSITPHTNFKAENVVLSKEEGGRHTPFFSNYRPQFYFRTTDTGVIELPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
      DN+++TVELISP+A+E GT+F+IREGGRTVG+GVVS+I
Sbjct: 356 DNIEMTVELISPIAIEDGTRFSIREGGRTVGSGVVSSI 393

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tr Q605B0 Translation elongation factor Tu [tuf-2] [Methylococcus 396
 Q605B0_METCA capsulatus] AA
align

Score = 563 bits (1452), Expect = e-159
 Identities = 279/400 (69%), Positives = 326/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIQTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 M+KEKE RT PHVN+GTIGHV HOKTTL+AA++ ++ K E K YD ID AP+E+ RG
 Sbjct: 1 MSKEKFTRTKPHVNVGTIGHVDHGKTTLTAAITKCKMAAKFGGEFKAYDQIDAAPEERARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120
 ITIAT+H+EYE+ RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI
 Sbjct: 61 ITIATAHVEYESAARHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+IVVFLNK S Y+FPGDD PI+ GSAL+ALE
 Sbjct: 121 LLARQVGVPPIVFLNKADMVDDPELLELVEMEVRELLSKYDFPGDDIPIIKGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AE-VDSYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTGRIER 239
 G+ E G ++ + + +D YIP PER ++ FLMP+EDVFSI+GRGT VVTGR+ER
 Sbjct: 181 ----GDGSEIGVPAVEALVQALDDYIPEPERAIDRPFMLPIEDVFSISGRGT VVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G++KVG+E+EIIVGIR T KTT TGVEMFRK L++G+AGDN+GVLLRGTK+E+VERG VL
 Sbjct: 237 GIIKVGEEIEIVGIRPTAKTTCTGVEMFRKLLDQGGAGDNIGVLLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYRPPQFYVRTT DVTGSITLPEGVEMVMPG 359
 KPGSITPH FE EIIYVLSKEEGGRHTPEE YRPQFY RTTDTVG++TLPEGVEMVMPG
 Sbjct: 297 KPGSITPHTHFEAEIYVLSKEEGGRHTPFFNGYRPPQFYFRTT DVTGAVTLPEGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNVKI V+LI+P+A++ G +PA+REGGRTVGAGVVS ILE
 Sbjct: 357 DNVKIEVKLIAPIAMDEGLRFAVREGGRTVGAGVVSNIIE 396

tr Q8EK70 Translation elongation factor Tu [tufA] [Shewanella 394
 Q8EK70_SHEON oneidensis] AA
align

Score = 563 bits (1450), Expect = e-159
 Identities = 278/398 (69%), Positives = 320/398 (79%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIQTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KE R+ PHVN+GTIGHV HOKTTL+AAIS VL+ E KD+ IDNAP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNVGTIGHVDHGKTTLTAAISHVLAKTYGGEAKDFSQIDNAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120
 ITI TSHIEY+T +RHYAHVDCPGHADVKNMITGAAQMDGAILVV++ DGMPMPQTREHI
 Sbjct: 61 ITINTSHIEYDTPSRHYAHVDCPGHADVKNMITGAAQMDGAILVVASTDGMPMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP I+VF+NK S Y+FPGDD P++ GSAL+ALE
 Sbjct: 121 LLSRQVGVPFIIVFMNKC DVMDDAE LLELVEMEVRELLSEYDFPGDDLPIVIGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTGRIER 240
 EW K+L+L A +DSYIP PERD +K FLMP+EDVFSI+GRGT VVTGR+ERG

Sbjct: 181 GEP-----EWEAKILELAAALDSYIPEPERDIDKPFLMPIEDVFSISGRGTVVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +V+VGDEVEIVGIR T KTT TGVEMFRK L++G AG+N G+LLRGTk+++VERG VL K

Sbjct: 236 IVRVGDEVEIVGIRTTTCTCTGVEMFRKLLDEGRAGENC GILLRGTKRDDVERGQVLSK 295

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFFTNYRPOFYVRTTDDVTGSITLPEGVEMVMPGD 360
 PGSI PH FE E+YVLSKEEGGRHTPFF YRPOFY RTTDDVTG+I LPEGVEMVMPGD

Sbjct: 296 PGSINPHTTFESEVYVLSKEEGGRHTPFFKGYRPOFYFRTTDDVTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
 N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ II

Sbjct: 356 NIKMVVTLICPIAMDEGLRFAIREGGRTVGAGVVAKII 393

tr Q7TT91 Elongation factor Tu [tufA] [Bordetella 396 AA
 Q7TT91_BORPE pertussis] align

Score = 563 bits (1450), Expect = e-159
 Identities = 285/400 (71%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K E + YD ID AP+EK RG

Sbjct: 1 MAKGKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLSNKFGEARGYDQIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI TSH+EXETETRHYAHVDCPGHADYVENMITGAAQMDGAILVVSADGMPQTREHI

Sbjct: 61 ITINTSHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+I+VELNK S Y+FPGDDTPIV GSA ALE

Sbjct: 121 LLSRQVGVPYIIIVFLNKADMVDDAELELVEMEVRELLSKYDFPGDDTPIVKGSAKLAL 180

Query: 181 EAKAGNVGEWGEK-VLKILMAEVD SYIPTPERDTEKTF LMPVEDVFSIAGRGTVVTGRIER 239
 G+ GE GE+ +L L +D+YIPTPER + FLMPVEDVFSI+GRGTVVVTGRIER

Sbjct: 181 ----GDKGELGEQAILS LAQALDYIPTPERAVDGAFLMPVEDVFSISGRGTVVVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 GVVKVG+E+IVGI+ T KTT TGVEMFRK L++G+AGDNVG+LLRGTk+E+VERG VL

Sbjct: 237 GVVKVGEEIEIVGIKPTVKTCTCTGVEMFRKLLDQGGAGDNV GILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEEEIYVLSKEEGGRHTPFFFTNYRPOFYVRTTDDVTGSITLPEGVEMVMPG 359
 KPGSI PH F E+Y+LSKEEGGRHTPFF YRPOFY RTTDDVTG+I LP EMV+PG

Sbjct: 297 KPGSINPHTDFTA EVYILSKEEGGRHTPFFNGYRPOFYFRTTDDVTGTIDL PADKEMVLPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV +TV+L++P+A+E G +FAIREGGRTVGAGVV+ II+

Sbjct: 357 DNVSM TVKLLAPIAMEEGLRFAIREGGRTVGAGVVAKI 396

tr Q79GC6 Elongation factor Tu [tuf] [Bordetella parapertussis] 396 AA
 Q79GC6_BORPA align

Score = 563 bits (1450), Expect = e-159

Identities = 285/400 (71%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K   E + YD ID AP+EK RG
Sbjct: 1  MAKGKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLSNKFGEARGYDQIDAAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI TSH+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI
Sbjct: 61  ITINTSHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+I+VFLNK                               S Y+FPGDDTPIV GSA ALE
Sbjct: 121  LLSRQVGVPYIIIVFLNKADMVDDAELLELVEMEVRELLSKYDFPGDDTPIVKGSAKLAL 180

Query: 181  EAKAGNVGEWGEK-VLKLMAEVD SYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIER 239
      G+ GE GE+ +L L   +D+YIPTPER +   FLMPVEDVFSI+GRGT VVTGRIER
Sbjct: 181  ----GDKGELGEQAILS LAQALD TYIPTPERAVDGAFLMPVEDVFSISGRGT VVTGRIER 236

Query: 240  GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      GVVKVG+E+EI VGI+ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL
Sbjct: 237  GVVKVGEEIEIVGIKPTVKTCTGVEMFRKLLDQGGAGDNVGILLRGTKREDVERGQVLA 296

Query: 300  KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPG 359
      KPGSI PH F   E+Y+LSKEEGGRHTPFF YRPQFY RTT DVTG+I LF   EMV+PG
Sbjct: 297  KPGSINPHTDFTA EVYILSKEEGGRHTPFFNGYRPQFYFRTT DVTGTIDL PADKEMVLP 356

Query: 360  DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNV +TV+L++P+A+E G +FAIREGGRTVGAGVV+ II+
Sbjct: 357  DNVSM TVKLLAPIAMEEGLRFAIREGGRTVGAGVVAKI I K 396

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tr Q79G84      Elongation factor Tu [tuf] [Bordetella bronchiseptica] 396
Q79G84_BORBR (Alcaligenes bronchisepticus)] AA
align

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Score = 563 bits (1450), Expect = e-159

Identities = 285/400 (71%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K   E + YD ID AP+EK RG
Sbjct: 1  MAKGKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLSNKFGEARGYDQIDAAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI TSH+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI
Sbjct: 61  ITINTSHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+I+VFLNK                               S Y+FPGDDTPIV GSA ALE
Sbjct: 121  LLSRQVGVPYIIIVFLNKADMVDDAELLELVEMEVRELLSKYDFPGDDTPIVKGSAKLAL 180

Query: 181  EAKAGNVGEWGEK-VLKLMAEVD SYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIER 239
      G+ GE GE+ +L L   +D+YIPTPER +   FLMPVEDVFSI+GRGT VVTGRIER
Sbjct: 181  ----GDKGELGEQAILS LAQALD TYIPTPERAVDGAFLMPVEDVFSISGRGT VVTGRIER 236

Query: 240  GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      GVVKVG+E+EI VGI+ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL

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Sbjct: 237 GVVKVGEEIEIVGIKPTVKTCTGVEMFRKLLDQGGAGDNVIGILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIEIVLSKEEGGRHTPFFTNYPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPGSI PH F E+Y+LSKEEGGRHTFFF YRPQFY RTTDVTG+I LF EMV+PG

Sbjct: 297 KPGSINPHTDFTAENVYILSKEEGGRHTPFFNGYRPFYFRTTDVTGTIDLPAKEMVLP 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV +TV+L++P+A+E G +FAIREGGRTVGAGVV+ II+

Sbjct: 357 DNVSMTVKLLAPIAMEEGLRFAIREGGRTVGAGVVAKI 396

tr Q5GWR8 Elongation factor Tu [tufB] [*Xanthomonas oryzae* (pv. 396
 Q5GWR8_XANOR *oryzae*)] AA
align

Score = 563 bits (1450), Expect = e-159
 Identities = 281/400 (70%), Positives = 327/400 (81%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PHVN+GTIGHV HGKTTL+AA++ + + + E K YD ID AP+EK RG

Sbjct: 1 MAKAKFERTKPHVNVGTIGHVDHGKTTLTAAITKIGAERFGGEFKAYDAIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAAAGPMPQTREHI 120
 ITI+T+H+EYE+ +RHYAHVDCPGHADVKNMITGAAQMDGAILV SAAGPMPQTREHI

Sbjct: 61 ITISTAHVEYESPSRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAAGPMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVPPIVFLNK S Y+EPGDDTPI+ GSA AL+

Sbjct: 121 LLSRQVGVPPIVFLNKADMVDDAELLELVEMEVRELLSKYDFPGDDTPIIHGSARLALD 180

Query: 181 EAKAGNVGEWG-EKVLKLMAEVDYSIPTPERDTEKTFMLPVEDVFSIAGRGTVVVGRIER 239
 G+ E G +LKL+ +D++IP P RD ++ FLMPVEDVFSI+GRGTVVVGRIER

Sbjct: 181 ----GDQSEIGVPAILKLVDALDTFIPEPTRDVRPFLMPVEDVFSISGRGTVVVGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G++KVGDE+EIVGIRATQKTTVTGVEMFR L++G+AGDN G+LLRGTK+++VERG VLC

Sbjct: 237 GIIKVGDEIEIVGIRATQKTTVTGVEMFRKLLDQGGAGDNAGLLLRGTRDDVERGQVLC 296

Query: 300 KPGSITPHKKFEEIEIVLSKEEGGRHTPFFTNYPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPGSI PH +FE E+YVLSK+EGGRHTFFF YRPQ Y RTTD+TG+I LPEGVEMVMPG

Sbjct: 297 KPGSIKPHTFEAEVYVLSKDEGGGRHTPFFKGYRPLYFRTTDITGAIDLPEGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNVK+TV LI+EVA++ G +FAIREGGRTVGAGVVS II+

Sbjct: 357 DNVKMTVTLINPVAMDEGLRFAIREGGRTVGAGVVSIIK 396

sp P43926 Elongation factor Tu (EF-Tu) [tufA] [*Haemophilus* 393
 EFTU_HAEIN *influenzae*] AA
align

Score = 562 bits (1448), Expect = e-159
 Identities = 275/398 (69%), Positives = 321/398 (80%), Gaps = 5/398 (1%)

Query: 2 AKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERGI 61

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+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+      + +D IDNAP+EK RGT
Sbjct: 1  SKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKHYGGAARAFDQIDNAPEEKARGI 60

Query: 62  TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHIL 121
          TT TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHIL
Sbjct: 61  TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHIL 120

Query: 122  LSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALEE 181
          L RQVGVP+I+VFLNK                      S Y+FPGDDTPIV GSAL+AL
Sbjct: 121  LGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRLLSQYDFPGDDTPIVRGSALQALN- 179

Query: 182  AKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 241
          V EW EK+L+L +D+YIF PER ++ FL+P+EDVFSI+GRGTVVTGR+ERG+
Sbjct: 180  ----GVAEWEKILELANHLDTYIPEPERAIDQPFLLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242  VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301
          ++ GDEVEIVGI+ T KTTVTGVEMFRK L++G AG+N+G LLRGT+EE+ERG VL KP
Sbjct: 236  IRTGDEVEIVGIKDTAKTTVTGVEMFRKLLDEGRAGENIGALLRGTKREEIERGQVLAKP 295

Query: 302  GSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGDN 361
          GSITPH FE E+YVLSK+EGGRHTPFF YRPQFY KTTDVTG+I LPEGVEMVMPGDN
Sbjct: 296  GSITPHTDFESEVYVLSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGDN 355

Query: 362  VKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
          +K+TV LI P+A++ G +FAIREGGRTVGAGVV+ II+
Sbjct: 356  IKMTVSLIHPIAMDQGLRFAIREGGRTVGAGVVAKIIE 393

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sp P57966      Elongation factor Tu-B (EF-Tu-B) [tufB] [Pasteurella] 394
EFTU2_PASMU multocida] AA
align

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Score = 561 bits (1447), Expect = e-159
Identities = 275/399 (68%), Positives = 322/399 (79%), Gaps = 5/399 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
          M+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+      + +D IDNAP+EK RG
Sbjct: 1  MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKHYGGAARAFDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
          ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI
Sbjct: 61  ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
          LL RQ+GV +I+VFLNK                      S Y+FPGDDTPIV GSAL+AL
Sbjct: 121  LLGRQIGVAYIIIVFLNKCDMVDDEELLELVEMEVRLEFSQYDFPGDDTPIVRGSALQALN 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
          V EW EK+L+L +D+YIP P+R ++ FL+P+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181  -----GVAEWEKILELANHLDTYIPEPQRAIDQPFLLPIEDVFSISGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
          +++ G+VEVEIVGI+AT KTTVTGVEMFRK L++G AG+N+G LLRGT+EE+ERG VL K
Sbjct: 236  IIRTGEEVEIVGIKATKTTVTGVEMFRKLLDEGRAGENVGALLRGTKREEIERGQVLAK 295

Query: 301  PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360

```

POSITPR FE E+YVLSKEEGGRATPEE YRPQFY RTTDVTEG+I LPEGVEMVMPGD
 Sbjct: 296 PGSITPHTDFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTTDDVTGTIELPEGVEMVMPGD 355
 Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 N+K+TV LI P+A++ G +FAIREGGRTVGAGVV+ II+
 Sbjct: 356 NIKMTVSLIHPIAMDQGLRFAIREGGRTVGAGVVAKIIK 394

tr Q65PA9 TufA (Elongation factor Tu) [tufA] [Bacillus 396
 Q65PA9_BACLD licheniformis (strain AA
 DSM 13 / ATCC 14580)] align

Score = 561 bits (1447), Expect = e-159
 Identities = 281/401 (70%), Positives = 326/401 (81%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLK-GLAEMKDYDNIDNAPQEKER 59
 MAKEKFF+R+ R NIGTIGHV HGKTTL+AAI+ VL K G YD ID AP+E+ER
 Sbjct: 1 MAKEKFDRSKSHANIGTIGHVDHGKTTLTAAITTVLHKKSGKGTAMAYDQIDGAPEERER 60
 Query: 60 GITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREH 119
 GITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREN
 Sbjct: 61 GITISTAHVEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREH 120
 Query: 120 ILLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRAL 179
 ILLSR VGVP+IVVFLNK S YEFPGDD P++ GSAL+AL
 Sbjct: 121 ILLSRNVGVPYIIVFLNKCDMVDDEELLELVEMEVRDLLSEYEFPGDDVPVIKGSALKAL 180
 Query: 180 EEAKAGNVGEWGEKVLKMAEVD SYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239
 E ++ EK+ +LMA VD YIPPER+T+K F+MPVEDVFSI GRGTV TGR+ER
 Sbjct: 181 E-----GDAQYEEKIFELMAAVDEYIPTPERETDKPFMPVEDVFSITGRGTVATGRVER 235
 Query: 240 GVVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298
 G VKVGDEVEI+G++ +KTTVTGVEMFRK L+ EAGDN+G LLRG +EE++RG VL
 Sbjct: 236 GQVKVGDEVEIIGLQEENKKTTVTGVMFRKLLDYAEAGDNIGALLRGVSREEIQRGQVL 295
 Query: 299 CKPGSITPHKKFEEEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMP 358
 +PG+ITPHKKF+ E+YVLSKEEGGRHTPFF+NYRPQFY RTTDVTEG I LPEGVEMVMP
 Sbjct: 296 AQPGTITPHKKFKAENVYVLSKEEGGRHTPFFSNYRPQFYFRTTDDVTGIIQLPEGVEMVMP 355
 Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 GDN+++TVELIS +A+E GT+F+IREGGRTVG+GVVS+IIE
 Sbjct: 356 GDNIEMTVELISTIAIEDGTRFSIREGGRTVGSGVVSSIIE 396

sp P33169 Elongation factor Tu (EF-Tu) [tuf] [Shewanella 394
 EFTU_SHEPU putrefaciens AA
 (Pseudomonas putrefaciens)] align

Score = 561 bits (1445), Expect = e-158
 Identities = 276/398 (69%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKER 60
 MAK KF R PHVN+GTIGHV HGKTTL+AAIS VL+ E KD+ IDNAP+E+ERG
 Sbjct: 1 MAKAKFERIKPHVNVGTIGHVDHGKTTLTAAISHVLAKTYGGEAKDFSQIDNAPEERER 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI TSHIEY+T +RHYAHVDCPGHADYVKNMITGAAQMDGAILVV++ DGMPQTREHI
 Sbjct: 61 ITINTSHIEYDTPSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVASTDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP I+VF+NK S Y+FPGDD P++ GSAL+ALE
 Sbjct: 121 LLSRQVGVPFIIVFMNKCDDVDEELLELVEMEVRELLSEYDFPGDDLPIVIGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
 EW K+L+L A +DSYIP P+RD +K FL+P+EDVESI+GRGT VVTGR+ERG
 Sbjct: 181 GEP-----EWEAKILELAAALDSYIPEPQRDIDKPFLLPIEDVFSISGRGT VVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +V+VGDEVEIVG+RAT KTT TGVEMFRK L++G AG+N G+LLRGTK+++VERG VL K
 Sbjct: 236 IVRVGDEVEIVGVRATTCTTCTGVEMFRKLLDEGRAGENC GILLRGTKRDDVERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTVGSITLPEGVEMVMPGD 360
 PGSI PH FE E+YVLSKEEGGRHTPFF YRPQFY RTTDTVG+I LPEGVEMVMPGD
 Sbjct: 296 PGSINPHTTFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTTDTVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
 N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ II
 Sbjct: 356 NIKMVVTLICPIAMDEGLRFAIREGGRTVGAGVAKII 393

tr Q8EK81 Translation elongation factor Tu [tufB] [Shewanella] 394
Q8EK81_SHEON oneidensis AA
align

Score = 561 bits (1445), Expect = e-158
 Identities = 277/397 (69%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KE R+ PHVN+GTIGHV HGKTTLSAAIS VL+ E KD+ IDNAP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNVGTIGHVDHGKTTLTAAISHVLAKTYGGEAKDFSQIDNAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI TSHIEY+T +RHYAHVDCPGHADYVKNMITGAAQMDGAILVV++ DGMPQTREHI
 Sbjct: 61 ITINTSHIEYDTPSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVASTDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP I+VF+NK S Y+FPGDD P++ GSAL+ALE
 Sbjct: 121 LLSRQVGVPFIIVFMNKCDDVDAELLELVEMEVRELLSEYDFPGDDLPIVIGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
 EW K+L+L A +DSYIP PERD +K FLMP+EDVESI+GRGT VVTGR+ERG
 Sbjct: 181 GEP-----EWEAKILELAAALDSYIPEPERDIDKPFLLPIEDVFSISGRGT VVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +V+VGDEVEIVGIR T KTT TGVEMFRK L++G AG+N G+LLRGTK+++VERG VL K
 Sbjct: 236 IVRVGDEVEIVGIRTTTCTTCTGVEMFRKLLDEGRAGENC GILLRGTKRDDVERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTVGSITLPEGVEMVMPGD 360
 PGSI PH FE E+YVLSKEEGGRHTPFF YRPQFY RTTDTVG+I LPEGVEMVMPGD
 Sbjct: 296 PGSINPHTTFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTTDTVTGIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
 N+N+ V LL P+A++ G +FAIREGGRTVGAGVV+ I
 Sbjct: 356 NIKMKVTLICPIAMDEGLRFAIREGGRTVGAGVVAKI 392

tr Q5NQ65 Translation elongation factor [ZM00516] [Zymomonas 397
 Q5NQ65_ZYMMO mobilis] AA
align

Score = 561 bits (1445), Expect = e-158
 Identities = 283/400 (70%), Positives = 326/400 (80%), Gaps = 4/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAE-MKDYNIDNAPQEKER 59
 MAK KF R FH NIGTIGHV HGKTTL+AAI+ VL+ G DY NID AP+E+ER
 Sbjct: 1 MAKAKFERNKPHCNIGTIGHVDHGKTTLTAAITKVLAEAGGGNTFVDYANIDKAPEERER 60

Query: 60 GITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREH 119
 GITI+TSH+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREH
 Sbjct: 61 GITISTSHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREH 120

Query: 120 ILLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRAL 179
 ILL+RQVGVP +VVF+NK S+Y+FPGDD PIV GSAL AL
 Sbjct: 121 ILLARQVGVPALVVF MNKVDQVDDPELLELVEMEIRELLSSYDFPGDDIPIVKGSALAAL 180

Query: 180 EEAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIER 239
 E+ K +G+ E +L LMA VD YIP PER +K+FLMP+EDVFSI+GRGT VVTGR+E
 Sbjct: 181 ED-KNPEIGK--EAILSLMAAVDEYIPQPERPLDKSFLMPIEDVFSISGRGT VVTGRVET 237

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+VKVG+EVEIVG+K T+KTTVTGVEMFRK L++G+AGDN+G LLRGT + EVERG VL
 Sbjct: 238 GIVKVGEEVEIVGLRDTKKT TTVTGVEMFRKLLDQGGAGDNIGALLRG TARTEVERGQVLA 297

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPOFYVRTT DVTGSITLPEGVEMVMPG 359
 KPGSITPH +F+ E+YVLSK+EGGRHTPFF NYRFQFY RTT DVTG ITLFE VEMVMPG
 Sbjct: 298 KPGSITPHTEFKA EYVLSKDEGGRHTPFFANYRPOFYFRTT DVTGEITLPEDVEMVMPG 357

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+ V+LI+P+A++ G +FAIREGGRTVGAGVVS+II+
 Sbjct: 358 DNIAFGVKLIAPIAMDPGLRFAIREGGRTVGAGVVSIIK 397

sp Q8CQ81 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus 394
 EFTU_STAEP epidermidis] AA
align

Score = 560 bits (1444), Expect = e-158
 Identities = 276/399 (69%), Positives = 320/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKF+R+ H NIGTIGHV HGKTTL+AAI+ VL+ G + YD IDNAP+EKERG
 Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDTVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI T+HIEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG ILVVSADGMPQTREHI
 Sbjct: 61 ITINTAHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVP HIVVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSR VGVP +VVELNK S Y+FPGDD P++AGSAL+ALE
 Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDDEELLELVEMEVRLDLSYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
 E+ +K+L IM VD YITPERD++K F+MPVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GDAEYEQKILDLMQAVDDYIPTPERDS DKPFMPVEDVFSITGRGT VATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +KVG+EVEL+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL
 Sbjct: 236 QIKVGEEVEIIGMHETS KTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYR PQFYVRTT DVTGSITLPEGVEMVMPGD 360
 PGSITPH KF+ E+YVLSK+EGGRHTPFFTNYR PQFY RTTDTG + LPEG EMVMPGD
 Sbjct: 296 PGSITPHTKFKA EVYVLSKDEGGRHTPFFTNYR PQFYFR TTDVTGVVNLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ I E
 Sbjct: 356 NVENTVELI APIAIEDGTRFSIREGGRTVGSGVVTEIFE 394

sp P33167 Elongation factor Tu (EF-Tu) [tuf] [Burkholderia cepacia] 396 AA
 EFTU_BURCE (Pseudomonas cepacia)]
align

Score = 560 bits (1444), Expect = e-158
 Identities = 282/400 (70%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ K E K YD ID AP+EK RG
 Sbjct: 1 MAKGKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLTKKFGGEAKAYDQIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120
 ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILV SAADGMPMPQTREHI
 Sbjct: 61 ITINTAHVEYETANRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGMPMPQTREHI 120

Query: 121 LLSRQVGVP HIVVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP+I+VFLNK S Y+FPGDDTPIV GSA ALE
 Sbjct: 121 LLARQVGVPYIIVFLNKCDSDDAELLELVEMEVRELLSKYDFPGDDTPIVKGSAKLAL 180

Query: 181 EAKAGNVGEWGEKVLKLM AE-VDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIER 239
 G+ GE GE + +A+ +D+YITPER + FLMPVEDVFSI+GRGT VVTGR+ER
 Sbjct: 181 ----GDTGELGEVAIMSLADALDYIPTPERAVDGAFLMPVEDVFSISGRGT VVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+VVKVG+E+ELVGT+ T KTT TGVEMFRK L++G+AGENVG+LLRGTK+E+VERG VL
 Sbjct: 237 GIVKVGEEIEIVGIKPTVKTCTGVEMFRKLLDQGGAGDNV GILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYR PQFYVRTT DVTGSITLPEGVEMVMPG 359
 KPGSITPH F E+YVLSK+EGGRHTPFF NYR PQFY RTTDTGSI LP+ EMVMPG
 Sbjct: 297 KPGSITPHTFTA EVYVLSKDEGGRHTPFFNNYR PQFYFR TTDVTGSIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ I++
 Sbjct: 357 DNVSITVKLI APIAMEEGLRFAIREGGRTVGAGVAKILD 396

tr Q5HRK4 Translation elongation factor Tu [tuf] [Staphylococcus 394
 Q5HRK4_STAEQ epidermidis AA
 (strain ATCC 35984 / RP62A)] align

Score = 560 bits (1444), Expect = e-158
 Identities = 276/399 (69%), Positives = 320/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAKEKF+R+ H NIGTIGHV HCKTTL+AAI+ VL+ G + YD IDNAP+EKERG
 Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTTLTAAIATVLAKNGDTVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI T+HIEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGMPQTREHI
 Sbjct: 61 ITINTAHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSR VGVP +VVFLNK S Y+FPGDD P++AGSAL+ALE
 Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
 E+ +K+L IM VD YLPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GDAEYEQKILDLMQAVDDYIPTPERDSKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL
 Sbjct: 236 QIKVGEEVEIIGMHETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDEVQRGQVLAA 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSITPH KF+ E+YVLSK+EGGRHTPFFTNYRPQFY RTTDVTG + LPEG EMVMPGD
 Sbjct: 296 PGSITPHTKFAEVYVLSKDEGGRHTPFFTNYRPQFYFRTTDVTGVVNLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ I E
 Sbjct: 356 NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIFE 394

sp Q9Z9L6 Elongation factor Tu (EF-Tu) [tuf] [Bacillus halodurans] 396 AA
 EFTU_BACHD align

Score = 560 bits (1443), Expect = e-158
 Identities = 279/399 (69%), Positives = 323/399 (80%), Gaps = 7/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLK-GLAEMKDYDNIDNAPQEKER 59
 MAKEKF+R+ H NIGTIGHV HCKTTL+AAI+ VL+ + G YD ID AP+E+ER
 Sbjct: 1 MAKEKFDRSKTHANIGTIGHVDHGKTTTLTAAITTVLAKRSGKGVAMAYDAIDGAPEERER 60

Query: 60 GITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREH 119
 GITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGMPQTREH
 Sbjct: 61 GITISTAHVEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREH 120

Query: 120 ILLSRQVGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRAL 179
 ILLSRQVGVP++VVFLNK S Y+FPGDD P++ GSAL+AL

Sbjct: 121 ILLSRQVGVPYLVVFLNKCDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVIRGSALKAL 180

Query: 180 EEAKAGNVGEWGEKVLKMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239
E EW EK+++LMA VD YIPTPERDTEK F+MPVEDVFSI GRGTV TGR+ER

Sbjct: 181 E-----GDAEWEEKIIEELMAAVDDYIPTPERDTEKPFMPVEDVFSITGRGTVATGRVER 235

Query: 240 GVVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298
G + VGDEVEI+G+ +KTTVTGVEMFRK L+ EAGDN+G LLRG +EEV+RG VL

Sbjct: 236 GQLNVGDEVEIIGLEEEAKKTTVTGVEMFRKLLDYAEAGDNIGALLRGVSREEVQRGQVL 295

Query: 299 CKPGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDVTGSITLPEGVEMVMP 358
KPG+ITPH F+ E+YVLSKEEGGRHTPEFF+NYRPQFY RTTDVTG I LP+GVEMVMP

Sbjct: 296 AKPGTITPHTNFKAENVYVLSKEEGGRHTPFSSNYRPQFYFRTTDVTGIIQLPDGVEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
GDNV++TVELI+P+A+E GTFK+IREGGRTVGAGVV++I

Sbjct: 356 GDNVEMTVELIAPIAIEEGTKFSIREGGRTVGAGVVASI 394

sp Q8NL22 Elongation factor Tu (EF-Tu) [tufA] [Xanthomonas 396
EFTU_XANAC axonopodis (pv. AA
citri)] align

Score = 560 bits (1442), Expect = e-158
Identities = 279/400 (69%), Positives = 325/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRNTNPVHNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
MAK KF RT PHVN+GTIGHV HGKTTL+AA++ + + + E K YD ID AP+EK RG

Sbjct: 1 MAKAKFERTKPHVNVGTIGHVDHGKTTLTAALTKIGAERFGGEFKAYDAIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120
ITL+T+H+EYE+ TRHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI

Sbjct: 61 ITISTAHVEYESPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
LLSRQVGVPPIVVFINK S Y+FPQDDTPI+ GSA AL+

Sbjct: 121 LLSRQVGVPPIVFLNKADMVDDAEELLELVEMEVRLLSKYDFPGDDTPIIHGSARIALD 180

Query: 181 EAKAGNVGEWG-EKVLKMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239
G+ + G +LKL+ +DS+IP P RD ++ FILMPVEDVFSI+GRGTVVTGRIER

Sbjct: 181 ----GDQSDIGVPAILKLVEALDSFIPEPTRDVRPFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
G++KVGDE+EIVGIR TQKTTVTGVEMFRK L++G+AGDN G+LLRGTK+++VERG VLC

Sbjct: 237 GIIVKVGDEIEIVGIRDTQKTTVTGVEMFRKLLDQGGAGDNAGLLLRGTRDDVERGQVLC 296

Query: 300 KPGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
KPGSI PH +FE E+YVLSK+EGGRHTPEFF YRPQFY RTTD+TG+ LPEGVEMVMPG

Sbjct: 297 KPGSIKPHTFEAEVYVLSKDEGGRHTPFFKGYRPQFYFRTTDITGACQLPEGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
DNVK+ V LI+PVA++ G +FAIREGGRTVGAGVV+ II+

Sbjct: 357 DNVKMVVTLINPVAMDEGLRFAIREGGRTVGAGVVAIIK 396

sp P33166 Elongation factor Tu (EF-Tu) (P-40) [tuf] [Bacillus 396
EFTU_BACSU subtilis] AA
align

Score = 560 bits (1442), Expect = e-158
Identities = 282/401 (70%), Positives = 320/401 (79%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIQTIGHVYHGKTTLSAAISAVLSLK-GLAEMKDYDNIDNAPQEKER 59
MAKEKE+R+ H NIQTIGHV HGKTTL+AAI+ VL K G YD ID AP+E+ER
Sbjct: 1 MAKEKFDRSKSHANIGTIGHVDHGKTTLTAAITTVLHKKSGKGTAMAYDQIDGAPEERER 60

Query: 60 GITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREH 119
GITI+T+H+EYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREH
Sbjct: 61 GITISTAHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREH 120

Query: 120 ILLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRAL 179
ILLS+ VGVP+IVVFLNK S Y+FFGDD P+V GSAL+AL
Sbjct: 121 ILLSKNVGVPYIVVFLNKCDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVVKGSALKAL 180

Query: 180 EEAKAGNVGEWGEKVLKILMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239
E EW K+ +LM VD YIPTPERDTEK F+MPVEDVFSI GRGTV TGR+ER
Sbjct: 181 E-----GDAEWEAKIFELMDAVDEYIPTPERDTEKPFMPVEDVFSITGRGTVATGRVER 235

Query: 240 GVVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298
G VVKVGDEVEI+G++ +KTTVTGVEMFRK L+ EAGDN+G LLRG +EE++RG VL
Sbjct: 236 GQVKVGDEVEIIGLQREENKKTTVTGVMFRKLLDYAEAGDNIGALLRGVSREEIQRGQVL 295

Query: 299 CKPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVTSITLPEGVEMVMP 358
KPG+ITPH KE+ E+YVLSKEEGGRHTPFF+NYRPQFY RTTDTVG I LPEGVEMVMP
Sbjct: 296 AKPGTITPHSKFKAEVYVLSKEEGGRHTPFFSNYRPQFYFRTTDTVTGIIHLPEGVEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
GDN ++ VELIS +A+E GT+F+IREGGRTVG+GVVS I E
Sbjct: 356 GDNTEMNVELISTIAIEEGTRFSIREGGRTVGSGGVVSTITE 396

sp P64029 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus 394
EFTU_STAAW (strain AA
MW2)] align

Score = 559 bits (1441), Expect = e-158
Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIQTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
MAKEKE+R+ H NIQTIGHV HGKTTL+AAI+ VL+ G + + YD IDNAP+EKERG
Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
ITI TSHIEY+T+ RHYAHVDCPGHADVKNMITGAAQMDG ILLVSAADGMPQTREHI
Sbjct: 61 ITINTSHIEYQTDKRHYAHVDCPGHADVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
LLSR VGVP +VVFLNK S Y+FFGDD P++AGSAL+ALE
Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKILMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
++ EK+L+IM VD+YIPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG

Sbjct: 181 -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGT VATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL

Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
 PGSITPH +F+ E+YVLSK+EGGRHTPFF+NYRPQFY RTTDDVTG + LPEG EMVMPGD

Sbjct: 296 PGSITPHTEFKAENVYVLSKDEGGGRHTPFFSNYRPQFYFRTTDDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+

Sbjct: 356 NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

sp Q6GBT9 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus] 394
 EFTU_STAAS (strain AA
 MSSA476)] align

Score = 559 bits (1441), Expect = e-158
 Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAKEKF+R+ H NIGTIGHV HGKTTL+AAI+ VL+ G + + YD IDNAP+EKERG

Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGPMPTREHI 120
 ITI TSHIEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG IIVVSAADGPMPTREHI

Sbjct: 61 ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSADGPMPTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSR VGVP +VVELNK S Y+FPGDD P++AGSAL+ALE

Sbjct: 121 LLSRNVGVPALVFLNKVDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
 ++ EK+L+LM VD+YIPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG

Sbjct: 181 -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGT VATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL

Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
 PGSITPH +F+ E+YVLSK+EGGRHTPFF+NYRPQFY RTTDDVTG + LPEG EMVMPGD

Sbjct: 296 PGSITPHTEFKAENVYVLSKDEGGGRHTPFFSNYRPQFYFRTTDDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+

Sbjct: 356 NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

sp Q6GJC0 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus] 394
 EFTU_STAAR (strain AA
 MRSA252)] align

Score = 559 bits (1441), Expect = e-158

Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
        MAKEKF+R+  H NIGTIGHV HGKTTL+AAI+ VL+  G +  + YD IDNAP+EKERG
Sbjct: 1  MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI TSHIEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG ILVSAADGMPQTREHI
Sbjct: 61  ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LLSR VGVP +VVFINK                      S Y+FPGDD P++AGSAL+ALE
Sbjct: 121  LLSRNVGVPALVVFLNKVDMVDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
        ++ EK+L+LM VD+YIPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300
        +KVG+EVEL+G+ T KTTVTGVMFRK L+  EAGDN+G LLRG +E+V+RG VL
Sbjct: 236  QIKVGEEVEIIGLHDTSKTTVTGVMFRKLLDYAEAGDNIGALLRGVAREDEVQRGQVLAA 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
        PGSITPH +P+ E+YVLSK+EGGRHTPFF+NYRPQFY RTTENVG + LPEG EMVMPGD
Sbjct: 296  PGSITPHTEFKAENVVLSKDEGGGRHTPFFSNYRPQFYFRTTDTVGVVHLPEGTEMVMPGD 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
        NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+
Sbjct: 356  NVENTVELIAPIAIEDGTRFSIREGGRTVGSGGVVTEIIK 394

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sp P99152      Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus 394
  EFTU_STAA   (strain
               N315)]
               align

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Score = 559 bits (1441), Expect = e-158

Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
        MAKEKF+R+  H NIGTIGHV HGKTTL+AAI+ VL+  G +  + YD IDNAP+EKERG
Sbjct: 1  MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI TSHIEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG ILVSAADGMPQTREHI
Sbjct: 61  ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LLSR VGVP +VVFINK                      S Y+FPGDD P++AGSAL+ALE
Sbjct: 121  LLSRNVGVPALVVFLNKVDMVDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
        ++ EK+L+LM VD+YIPTPERD++K F+MPVEDVEST GRGTV TGR+ERG
Sbjct: 181  -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300

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      +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL
Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDEVQRGQVLAA 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
      PGSITPH +F+ E+YVLSK+EGGRHTPEFF+NYRPQFY RTTDDVTG + LPEG EMVMPGD
Sbjct: 296 PGSITPHTEFKAENVYVLSKDEGGRHTPFFSNYPQFYFRTTDDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+
Sbjct: 356 NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

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sp P64028      Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus 394
  EFTU_STAAM (strain AA
      Mu50 / ATCC 700699)] align

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Score = 559 bits (1441), Expect = e-158
 Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

```

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAKEKF+R+ W NIGTIGHV HGTTL+AAI+ VL+ G + + YD IDNAP+EKERG
Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI TSHIEY+T+ RHYAHVDCPGHADVKNMITGAAQMDG ILLVVSADGMPQTREHI
Sbjct: 61 ITINTSHIEYQTDKRHYAHVDCPGHADVKNMITGAAQMDGGILVVSADGMPQTREHI 120

Query: 121 LLSRQGVGVPHIVVFLNKXXXXXXXXXXXXXXXXXXXXXAYEFPGDDTPIVAGSALRALE 180
      LLSR VGVP +VVFLNK S Y+FPGDD P++AGSAL+ALE
Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVTGRIERG 240
      ++ EK+L+IM VD+YIPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181 -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL
Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDEVQRGQVLAA 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
      PGSITPH +F+ E+YVLSK+EGGRHTPEFF+NYRPQFY RTTDDVTG + LPEG EMVMPGD
Sbjct: 296 PGSITPHTEFKAENVYVLSKDEGGRHTPFFSNYPQFYFRTTDDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+
Sbjct: 356 NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

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tr Q5HIC7      Translation elongation factor Tu [tuf] [Staphylococcus 394
  Q5HIC7_STAAC aureus AA
      (strain COL)] align

```

Score = 559 bits (1441), Expect = e-158
 Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      MAKEKF+R+  H NIQTIGHV HCKTTL+AAI+ VL+  G +  + YD IDNAP+EKERG
Sbjct: 1  MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI TSHIEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG ILLVSAADGMPQTREHI
Sbjct: 61  ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSR VGVF +VVELNK                               S Y+FPGDD P++AGSAL+ALE
Sbjct: 121  LLSRNVGVPALVVFLNKVMDVDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      .      ++ EK+L+LM VD+YIPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  -----GDAQYEEKILELMEAVDTYIPTPERDS DKPFMPVEDVFSITGRGT VATGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +KVG+EVEI+G+ T KTTVTGVEMFRK L+  EAGDN+G LIRG +E+V+RG VL
Sbjct: 236  QIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVTSITLPEGVEMVMPGD 360
      PGSITPH +F+ E+YVLSK+EGGRHTPFET+NYRPQFY RTTDTVTS + LPEG EMVMPGD
Sbjct: 296  PGSITPHTEFKAENVYVLSKDEGGRTPFSSNYRPQFYFRTTDTVGVVHLPEGTEMVMPGD 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+
Sbjct: 356  NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

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tr Q5QWA3 Translation elongation factor EF-Tu [tufB_1] [Idiomarina 394 AA
Q5QWA3_IDILO loihiensis]

align

Score = 559 bits (1441), Expect = e-158
Identities = 271/399 (67%), Positives = 325/399 (80%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      M+KEKF R+ PHVN+GTHGV HCKTTL+AAI+ VL+  KD+ IDNAP+EKERG
Sbjct: 1  MSKEKFERSKPHVNVGTIGHVDHGKTTLTAAITTVLAKVYGGAAKDFAAIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI+TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61  ITISTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP I VVF+NK                               S Y+FPGDD P++GSAL+ALE
Sbjct: 121  LLSRQVGVPFIVVFMNKCMDVDEELLELVEMEVRRELLSEYDFPGDDLPIVQGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      +      EW +K+++L +D+YIP PERD +K F+MP+EDVFSI+GRGT VVTGR+ERG
Sbjct: 181  GDE-----EWSKKIVELADALDNYIPEPERDIDKPFIMPIEDVFSISGRGT VVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +V+ GDE EIVG++ T KTTVTGVEMFRK L++G AG+N+G LIRGK+++VERG VL K
Sbjct: 236  IVRTGDECEIVGMKDTTKTTVTGVEMFRKLLDEGRAGENIGALLRGTKRDDVERGQVLAK 295

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Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
 PG+ITPH KFE E+YVLSK+EGGRHTPEE YRPQFY RTTDDVTG++ LPEGVEMVMPGD
 Sbjct: 296 PGTITPHTKFEAEVYVLSKDEGGRHTPFFKGYRPQFYFRTTDDVTGAVELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 N+K V+LI+P+A++ G +FAIREGGRTVGAGVVS I++
 Sbjct: 356 NLKFVVDLIAPIAMDEGLRFAIREGGRTVGAGVVSIMD 394

tr Q6N4Q4 **Elongation factor Tu (EC 3.6.1.48) [tuf/ EF-Tu]** 396
 Q6N4Q4_RHOPA **[Rhodopseudomonas** AA
palustris] align

Score = 558 bits (1439), Expect = e-158
 Identities = 280/401 (69%), Positives = 323/401 (79%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PH NIGTIGHV HGKT+L+AAI+ VL+ G A YD ID AP+EK RG
 Sbjct: 1 MAKAKFERTKPHCNIGTIGHVDHGKTSLTAAITKVLAEETGATFTAYDQIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAAGMPQTREHI 120
 ITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAAGMPQTREHI
 Sbjct: 61 ITISTAHVEYETQNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAAGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP +VVFLNK S Y+FPGDD PIV GSAL ALE
 Sbjct: 121 LLARQVGVPALVVFLNKCDDPELLELVEMEVRLLSKYDFPGDDIPVKGSAALALE 180

Query: 181 --EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVTGRIE 238
 +AK G+ + +L+LM +VD+YIP PER ++ FMPVEDVFSI+GRGTVVTGR+E
 Sbjct: 181 NSDAKLGH-----DAILELMRQVDAYIPQPERPIDQPFMPVEDVFSISGRGTVVTGRVE 235

Query: 239 RGVVKGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298
 RG++KVGDE+EIVGIR TQKTT TGVEMFRK L++G+AGDN+G LLRGTK+E+VERG VL
 Sbjct: 236 RGILKVGDEIEIVGIRDQKTTCTGVEMFRKLLDQGGAGDNIGALLRGTKREDVERGQVL 295

Query: 299 CKPGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMP 358
 CKPGS+ PH KF+ E Y+L+KEEGGRHTPFFFTNYRPQFY RTTDDVTG + LPEG EMVMP
 Sbjct: 296 CKPGSVKPHTKFAEAYILTKEEGGRHTPFFFTNYRPQFYFRTTDDVTGVVHLPEGTEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 GDN+ + V LI P+A+E +FAIREGGRTVGAGVV+ IIE
 Sbjct: 356 GDNIAEVHLIVPIAMEEKLRFIREGGRTVGAGVVAIIE 396

tr Q73F98 **Translation elongation factor Tu [tuf] [Bacillus cereus** 395
 Q73F98_BACC1 **(strain** AA
ATCC 10987)] align

Score = 558 bits (1439), Expect = e-158
 Identities = 275/400 (68%), Positives = 322/400 (79%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ G AE + YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITTVLAKAGGAEGYDQIDAAPEERERG 60


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Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGMPQTREHI
Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+IVVFLNK S Y FPGDD P++ GSAL+AL+
Sbjct: 121 LLSRQVGVPYIVVFLNKCDDMVDEELLELVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      +W K+++LMAEVD+YIPTPER+T+K FILMPVEDVFSI GRGTV TGR+ERG
Sbjct: 181 -----GEADWEAKIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      +VKGVD VEI+G+ TTVTGVEMFRK L++ +AGDN+G LARG +E+++RG VL
Sbjct: 236 IVKVGDVVEIIGLAEENASTTVTGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
      K GS+ H KF+ E++VLSKEEGGRHTPEF NYRPQFY RTTDTG I LPEG EMVMPG
Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDTGTIIQLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKEFAIREGGRTVGAGVVSNIIE 399
      DNV++T+ELI+P+A+E GTKE+IREGGRTVG GVV+ I+E
Sbjct: 356 DNVENTIELIPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

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sp Q814C4      Elongation factor Tu (EF-Tu) [tuf] [Bacillus cereus] 395
EFTU_BACCR (strain ATCC AA
14579 / DSM 31)] align

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Score = 558 bits (1438), Expect = e-158
 Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

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Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK KF R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ G AE + YD ID AP+E+ERG
Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITTVLAKAGGAEEARGYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGMPQTREHI
Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+IVVFLNK S Y FPGDD P++ GSAL+AL+
Sbjct: 121 LLSRQVGVPYIVVFLNKCDDMVDEELLELVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      +W K+++LMAEVD+YIPTPER+T+K FILMPVEDVFSI GRGTV TGR+ERG
Sbjct: 181 -----GEADWEAKIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      +VKGVD VEI+G+ TTVTGVEMFRK L++ +AGDN+G LARG +E+++RG VL
Sbjct: 236 IVKVGDVVEIIGLAEENASTTVTGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
      K GS+ H KF+ E++VLSKEEGGRHTPEF NYRPQFY RTTDTG I LPEG EMVMPG
Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDTGTIIQLPEGTEMVMPG 355

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Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+++T+ELI+P+A+E GTKF+IREGGRTVG GVV+ I+E
 Sbjct: 356 DNIEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

sp Q81VT2 Elongation factor Tu (EF-Tu) [tuf] [Bacillus anthracis] 395 AA
 EFTU_BACAN

align

Score = 558 bits (1438), Expect = e-158
 Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KF R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ G AE + YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITTVLAKAGGAEEARGYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGMPQTREHI
 Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVFLNK S Y FPGDD P++ GSAL+AL+
 Sbjct: 121 LLSRQVGVPPIVFLNKCDMVDDEELLELVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFIMPVEDVFSIAGRGTVTGRIERG 240
 +W K+++LMAEVD+YIPTPER+T+K FIMPVEDVFSI GRGTV TGR+ERG
 Sbjct: 181 -----GEADWEAKIIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 +VKEVD VEL+G+ TTVTGVEMFRK L++ +AGDN+G LLRG +E+++RG VL
 Sbjct: 236 IVKVGDVVEIIGLAEENASTTVTGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
 K GS+ H KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTEVTG I LPEG EMVMPG
 Sbjct: 296 KSGSVKAHAKFKAIEVFVLSKEEGGRHTPFFANYPQFYFRTTDTGTIIQLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+++T+ELI+P+A+E GTKF+IREGGRTVG GVV+ I+E
 Sbjct: 356 DNIEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

tr Q6HPR0 Protein-synthesizing GTPase (Translation elongation 395
 Q6HPR0_BACHK factor Tu AA
 (EF-TU)) (EC 3.6.5.3) [tufA] [Bacillus thuringiensis
 (subsp. konkukian)] align

Score = 558 bits (1438), Expect = e-158
 Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KF R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ G AE + YD ID AP+E+ERG
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITTVLAKAGGAEEARGYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

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      ITI+T+H+EYETETRHYAHVDCPGHADVKNMITGAAQMDG LLVVSADGMPQTREHI
Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGGILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+IVVFLNK                               S Y FPGDD P++ GSAL+AL+
Sbjct: 121 LLSRQVGVPPIVFLNKCDMVDDEELLELVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      +W K+++LMAEVD+YIPTPER+T+K FILMPVEDVFSI GRGTV TGR+ERG
Sbjct: 181 -----GEADWEAKIIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      +VVKVG D VEI+G+          TTVTGVEMFRK L++ +AGDN+G LLRG +E+++RG VL
Sbjct: 236 IVKVGDVVEIIGLAEENASTTVTGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPG 359
      K GS+ H KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTDDVTG I LPEG EMVMPG
Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDDVTGIIQLPEGTEMVMPG 355

Query: 360 DNVKITVELISPALELGTKFAIREGGRTVGAGVVSNIIE 399
      DN+++T+ELL+P+A+E GTEK+IREGGRTVG GVV+ I+E
Sbjct: 356 DNIEMTIELIPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

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tr Q63H92      Protein-synthesizing GTPase (Translation elongation      395
Q63H92_BACCZ factor Tu                                         AA
      (EF-TU)) (EC 3.6.5.3) [tufA] [Bacillus cereus (strain      align
      2K)]

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Score = 558 bits (1438), Expect = e-158

Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

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Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK KF R+ PHVNIGTIGHV HGKTTL+AAAL+ VL+ G AE + YD ID AP+E+ERG
Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITTVLAKAGGAEARGYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI+T+H+EYETETRHYAHVDCPGHADVKNMITGAAQMDG LLVVSADGMPQTREHI
Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGGILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+IVVFLNK                               S Y FPGDD P++ GSAL+AL+
Sbjct: 121 LLSRQVGVPPIVFLNKCDMVDDEELLELVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      +W K+++LMAEVD+YIPTPER+T+K FILMPVEDVFSI GRGTV TGR+ERG
Sbjct: 181 -----GEADWEAKIIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      +VVKVG D VEI+G+          TTVTGVEMFRK L++ +AGDN+G LLRG +E+++RG VL
Sbjct: 236 IVKVGDVVEIIGLAEENASTTVTGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300 KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPG 359
      K GS+ H KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTDDVTG I LPEG EMVMPG
Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDDVTGIIQLPEGTEMVMPG 355

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Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DN+++T+ELL+P+A+E GTEF+IREGGRTVG GVV+ I+E
 Sbjct: 356 DNIEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

tr Q6MJ00 Translation elongation factor Tu (EC 3.6.1.48) [tuf] 396
 Q6MJ00_BDEBA [Bdellovibrio 396
 bacteriovorus] align

Score = 557 bits (1436), Expect = e-157
 Identities = 275/400 (68%), Positives = 321/400 (79%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 M+KEKE R PHVNIGTIGHV HGKTTL+AAI+ L+ G A+ YD ID +P+EK RG
 Sbjct: 1 MSKEKFTRNKPHVNIGTIGHVDHGKTTLTAAITTTLAASGKAQAMAYDQIDKSPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVS+ADGMPQTREHI
 Sbjct: 61 ITISTTHVEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP +VVE+NK S YEFPGDD P+V GSAL+ALE
 Sbjct: 121 LLARQVGVPALVVFMMNKVDMVDDKELLELELVRELLSKYEFPGDDIPVVKGSALKALE 180

Query: 181 EAKAGNVGEWGEK-VLKLMAEVD SYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTGRIER 239
 G+ E G ++KLM D+YIP P R +KTFMLPVEDVFSI+GRGT VVTGR+ER
 Sbjct: 181 ----GDTSEIGRPAIMKLMEACDTYIPAPVRAVDKTFMLPVEDVFSISGRGT VVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+VKVGDE+ELVGIR TQKTTVTG+EMERK L++G+AGDN GVLLRGTKKE+VERG VL
 Sbjct: 237 GIVKVGDEIEIVGIRPTQKTTVTGIEMFRKLLDEGQAGDNCVLLRGTKKEDVERGQVLV 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPOFYVRTT DVTGSITLPEGVEMVMPG 359
 KPG++ PHKKF+ E Y+L+KEEGGRHTPFF YRPQFY RTTDTVTG TL G EMVMPG
 Sbjct: 297 KPGTVKPHKKFKAEAYILTKEEGGRHTPFFNGYRPOFYFRTT DVTGVCTLKAGTEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 D ++++VELI+P+A+E +FAIREGGRTVGAGVV+ I+E
 Sbjct: 357 DKIEVSVELIAPIAIEEKELRFAIREGGRTVGAGVVTEILE 396

tr Q9F9S8 Eftu [eftu] [EDTA-degrading bacterium 391 AA
 Q9F9S8_9PROT BNC1] align

Score = 557 bits (1435), Expect = e-157
 Identities = 284/399 (71%), Positives = 320/399 (80%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KF RT PHVNIGTIGHV HGKT+L+AAI+ K E K YD ID AP+EK RG
 Sbjct: 1 MAKGKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEEKARG 55

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI+T+H+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
 Sbjct: 56 ITISTAHVEYETENRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 115

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP I VFLNK S YEFPGDD PIV GSAL ALE
 Sbjct: 116 LLARQVGVPPIVFLNKVDQVDDPELLELVELEIRELLSKYEFPGDDIPVKGSAALAALE 175

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
 ++ +GE + V +LMAEVD YIPTER ++ FIMP+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 176 DSNK-EIGE--DAVRQLMAEVDKYIPTPERPIDQPFLMPIEDVFSISGRGTVVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 VVKVG+EVEIVGIR T KTTVTGVEMFRK L++G+AGDN+G LLRG +E VERG VL K
 Sbjct: 233 VVKVGEEVEIVGIRPTSKT TTVTGVEMFRKLLDQGGAGDNIGALLRGIDREGVERGQVLAK 292

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
 PGS+TPH KP+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTDTVGS +TLPEG EMVMPGD
 Sbjct: 293 PGSVTPHTKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTTDTVGVVTLPEGTEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV + V LI P+A+E +FAIREGGRTVGAG+V++I E
 Sbjct: 353 NVTMDVT LIVPIAMEERLRFAIREGGRTVGAGIVASITE 391

tr Q5PIW4 Elongation factor Tu [tufA] [Salmonella paratyphi-a] 394 AA
 Q5PIW4_SALPA

align

Score = 556 bits (1434), Expect = e-157

Identities = 272/398 (68%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 M+KEKE RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG
 Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI TSH+EY+T TRHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGMPQTREHI
 Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
 Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEURELLSQYDFPGDDTPIVRSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
 EW K++L +DSYIP PER +K EL+P+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 181 -----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 ++KVG+EVEIVGI+ TQK+T TGVMFRK L++G AG+NVGVLLRG K+EE+ERG VL K
 Sbjct: 236 IIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
 PG+I PH KFE E+Y+LSK+EGGRHTPEE YRPQFY RTTDTVGS+I LPEGVEMVMPGD
 Sbjct: 296 PGTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDTVGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 398
 N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
 Sbjct: 356 NIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVAKVL 393

tr Q57H76 Protein chain elongation factor EF-Tu (Duplicate of 394
 Q57H76_SALCH tufA) [tufB] AA
 [Salmonella cholerae-suis (Salmonella enterica)] align

Score = 556 bits (1434), Expect = e-157
 Identities = 272/398 (68%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 M+KEKEF RT PHVN+GTIGHV HGKTTL+AAAI+ VL+ + +D IDNAP+EK RG
 Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI TSH+EY+T TRHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGMPQTREHI
 Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
 Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
 EW K+++L +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 181 -----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 ++KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL K
 Sbjct: 236 IIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
 PG+I PH KFE E+Y+LSK+EGGRHTPF YRPQFY RTTDDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGTIKPHTKFESEVYILSKDEGGRHTPFKGYRPFYFRTTDDVTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
 N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
 Sbjct: 356 NIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 393

tr Q6N0C2 EF-Tu [orf3309] [Magnetospirillum 396 AA
 Q6N0C2_9PROT gryphiswaldense] align

Score = 556 bits (1434), Expect = e-157
 Identities = 280/399 (70%), Positives = 319/399 (79%), Gaps = 3/399 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KE R PH NIGTIGHV HGKT+L+AAAI+ VL+ G A YD ID AP+EK RG
 Sbjct: 1 MAKAKFERNKPHCNIGTIGHVDHGKTSLTAAITKVLAETGGATFTAYDQIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI+T+H+EYET PHXAHVDCPGHADVKNMITGAAQMDG ILLVSAADGMPQTREHI
 Sbjct: 61 ITISTAHVEYETANRHYAHVDCPGHADVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP +VVF+NK S+Y+FPGDD PIV GSAL ALE
 Sbjct: 121 LLARQVGVPALVVFVNKCDMVDDELLDLVELEVRELLSSYDFPGDDIPIVIRGSALCALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240

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      + K   +G   + +L LMAEVD YIP PER  +K FLMP+EDVFSI+GRGTVVTR+ERG
Sbjct: 181 D-KQPEIGR--DAILALMAEVDKYIPQPERPKDKPFLMPIEDVFSISGRGTVVTRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      VVKVG+EVEIVGI+ T KTT TGVEMFRK L++GEAGDN+G LLRG K+E+VERG VL
Sbjct: 238 VVKVGEEVEIVGIKPTVKTCTGVEMFRKLLDQGEAGDNIGALLRGVKREDVERGQVLAA 297

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
      PGSITPH KF E Y+L+KEEGGRHTPFFFTNYRPQFY RTTDDVTG + LPEG EMVMPGD
Sbjct: 298 PGSITPHTKFTAAYIILNKEEGGRHTPFFFTNYRPQFYFRTTDDVTGMVYLPEGTEMVMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      NV +TV+LL+P+A++ G +FAIREGGRTVGAGVV+ IIE
Sbjct: 358 NVSMTVQLIAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

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sp P26184      Elongation factor Tu (EF-Tu) [tuf] [Flexistipes]      396
      EFTU_FLESI sinusarabici]
                                     AA
                                     align

```

Score = 556 bits (1433), Expect = e-157
 Identities = 275/399 (68%), Positives = 325/399 (80%), Gaps = 3/399 (0%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      M+K+K+ R PHVN+GTIGHV HGKTTL+AA++ VLSLKG A+ ++ NID AP+EKERG
Sbjct: 1  MSKQKYERKKPHVNVGTIGHVDHGKTTLTAAATHVLSLKGYADYIEFGNIDKAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120
      ITIAT+H+EYE++ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI
Sbjct: 61 ITIATAHVEYESDKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP IVVF+NK + YEFPGDD PI+ GSAL+ALE
Sbjct: 121 LLARQVGVPISIVFMNKCMDVDEELLELEVEIRDLLNTYEFPGDDIPIKGSALQALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTRGRIERG 240
      A+ E + + +L+ +D YIP PERD +K FLMP+EDVFSI+GRGTVVTR+ERG
Sbjct: 181 NAEDE---EKTKCIWELLQAMDDYIPAPERDIDKPFLMPIEDVFSISGRGTVVTRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      V+V DE+EIVG+ T+KT VTGVEMFRK L++GEAGDNVGVLLRG KK++VERG VL K
Sbjct: 238 KVRVQDEIEIVGLTDTRKTVVTGVEMFRKILDEGEAGDNVGVLLRGIKKDDVERGQVLAK 297

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
      PGSITPH+KE+ E Y+L+KEEGGRHTPFF+ YRPQFY RTTDDVTG ITL EGVEVMPGD
Sbjct: 298 PGSITPHRKFKCEAYILTKEEGGRHTPFFSGYRPQFYFRTTDDVTGVITLAEGVEMVMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      N+ V+LI P+A+E G +FAIREGGRTVGAGVV+ I+E
Sbjct: 358 NISCDVDLIQPIAMEQGLRFAIREGGRTVGAGVVTEIVE 396

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sp Q83JC4      Elongation factor Tu (EF-Tu) [tufA] [Shigella flexneri] 393 AA
      EFTU_SHIFL
                                     align

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Score = 555 bits (1431), Expect = e-157
Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

Query:	2	AKEKFNRTNPNHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI	61
		+KEKF RT PRVN+GTIGHV HGTFTL+AAI+ VL+ + +D IDNAP+EK RGI	
Sbjct:	1	SKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI	60
Query:	62	TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILLVSAADGMPQTREHIL	121
		TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHIL	
Sbjct:	61	TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHIL	120
Query:	122	LSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE	181
		L RQVGVP+I+VFLNK S Y+FGDDTPIV GSAL+ALE	
Sbjct:	121	LGRQVGVPYIIVFLNKCDDVDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALE-	179
Query:	182	AKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG	241
		EW K+L+L +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG+	
Sbjct:	180	----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLLPIDVFSISGRGTVVTGRVERGI	235
Query:	242	VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP	301
		+KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL KP	
Sbjct:	236	IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENGVLLRGIKREEIERGQVLAKP	295
Query:	302	GSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGDN	361
		G+I PH KFE E+Y+LSK+EGGRHTFFF YRPQFY RTTDTVGS+I LPEGVEMVMPGDN	
Sbjct:	296	GTIKPHTKFESEVYILSKDEGGGRHTPFFKGYRPQFYFRTTDTVGTIELPEGVEMVMPGDN	355
Query:	362	VKITVELISPALELGTKFAIREGGRTVGAGVVSNI	398
		+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++	
Sbjct:	356	IKMVTTLIHPAMDDGLRFAIREGGRTVGAGVVAKVL	392

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sp   P0A6N1      Elongation factor Tu (EF-Tu) (P-43) [tufA] [Escherichia    393
      EFTU_ECOLI coli]
                                     AA
                                     align

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Score = 555 bits (1431), Expect = e-157
Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

Query: 2	AKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI	61
	+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ * +D IDNAP+EK RGI	
Sbjct: 1	SKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI	60
Query: 62	TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREHIL	121
	TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILLV+A DGMPMPQTREHIL	
Sbjct: 61	TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPMPQTREHIL	120
Query: 122	LSRQVGVPPIVFLNKKXXXXXXXXXXXXXXXXXXXXX SAYEFPGGDDTPIVAGSALRALEE	181
	L RQVGVP+I+VFLMK S Y+FPGGDDTPIV GSAL+ALE	
Sbjct: 121	LGRQVGVPYIIIVFLNKKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALE-	179
Query: 182	AKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG	241
	EW K+L+L +DSYIP PER +K FL+P+EDVFST+GRGTVVVGR+ERG+	
Sbjct: 180	----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLLPIDVFSISGRGTVVTGRVERGI	235
Query: 242	VKVGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP	301


```

+KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLIRG K+EE+ERG VL KP
Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPOFYVRTTDVTGSITLPEGVEMVMPGDN 361
G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPGDN
Sbjct: 296 GTIKPHTKFESSEVYILSKDEGGRHTPFFKGYRPOFYFRTTDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
Sbjct: 356 IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

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sp P0A6N2      Elongation factor Tu (EF-Tu) (P-43) [tufA] [Escherichia      393
EFTU_ECOL6 coli 06] AA
align

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Score = 555 bits (1431), Expect = e-157
Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

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Query: 2  AKEKFNRNTPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI 61
+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RGI
Sbjct: 1  SKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI 60

Query: 62  TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHIL 121
TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPTQREHIL
Sbjct: 61  TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPTQREHIL 120

Query: 122 LSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 181
L RQVGVP+I+VFLNK S Y+FPGDTPIV GSAL+ALE
Sbjct: 121 LGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRILLSQYDFPGDDTPIVRGSALKALE- 179

Query: 182 AKAGNVGEWGEKVLKMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVTGRIERG 241
EW K+L+L +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG+
Sbjct: 180 ----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCKP 301
+KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLIRG K+EE+ERG VL KP
Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPOFYVRTTDVTGSITLPEGVEMVMPGDN 361
G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDVTG+I LPEGVEMVMPGDN
Sbjct: 296 GTIKPHTKFESSEVYILSKDEGGRHTPFFKGYRPOFYFRTTDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
Sbjct: 356 IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

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sp P0A6N3      Elongation factor Tu (EF-Tu) (P-43) [tufA] [Escherichia      393
EFTU_ECO57 coli
0157:H7] AA
align

```

Score = 555 bits (1431), Expect = e-157
Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

```

Query: 2  AKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI 61
+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RGI
Sbjct: 1  SKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI 60

Query: 62  TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREHIL 121
TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPMPQTREHIL
Sbjct: 61  TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPMPQTREHIL 120

Query: 122  LSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 181
L RQVGVP+I+VELNK S Y+FPGDDTPIV GSAL+ALE
Sbjct: 121  LGRQVGVPYIIVFLNCKMVDDEELLELVEMEVRLLSQYDFPGDDTPIVRSALKALE- 179

Query: 182  AKAGNVGEWGEKVLKMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 241
EW K+L+L +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG+
Sbjct: 180  ----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242  VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301
+KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL KP
Sbjct: 236  IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENGVLLRGIKREEIERGQVLA KP 295

Query: 302  GSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPGDN 361
G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDTGTG+I LPEGVEMVMPGDN
Sbjct: 296  GTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPFYFRTTDTGTIELPEGVEMVMPGDN 355

Query: 362  VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
Sbjct: 356  IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

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tr Q5ZYP5 Translation elongation factor Tu (EF-Tu) (EC 3.6.5.3) 396
Q5ZYP5_LEGPH [tufB] AA
[Legionella pneumophila subsp. pneumophila (strain align
Philadelphia 1 / ATCC 33152)]

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Score = 555 bits (1430), Expect = e-157
Identities = 278/400 (69%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI 60
MAKEKF R PHVN+GTIGHV HGKTTL+AAI+ +++ K K YD ID AP+E+ERG
Sbjct: 1  MAKEKFERKKPHVNVGTIGHVDHGKTTLTAAITTIMAKKYGGTAKAYDQIDAAPEERERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120
ITI+T+H+EYE+ +RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREHI
Sbjct: 61  ITISTAHVEYESASRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 180
LLSRQVGVP+IVVF+NK S+Y+FPGDD PIV GSAL+ALE
Sbjct: 121  LLSRQVGVPYIIVFMNKADMVDDPELLELVEMEVRDLLSSYDFPGDDIPIVGSALKALE 180

Query: 181  EAKAGNVGEWGEKVL-KLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIER 239
G + G K + KL+ +DSYIP R R+ +K FL+P+EDVFSI+GRGTVVTGR+E
Sbjct: 181  ----GEDSDIGVKAIEKLVETMSYIPEPVRNIDKPFLLPIEDVFSISGRGTVVTGRVES 236

Query: 240  GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
G+KVG+EVEIVGIR TQKTT TGVEMFRK L++G AGDNVGVLLRGTK++EVERG VL
Sbjct: 237  GIVKVGEEVEIVGIRDITQKTTCTGVEMFRKLLDEGRAGDNVGVLLRGTKRDEVERGQVLA 296

```

Query: 300 KPGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPG+I PH KFE E+YVLSKEEGGRHTEFF YRPQFY RTTDVTG+ LP GVEMVMPG
 Sbjct: 297 KPGTIKPHTKFEAEVYVLSKEEGGRHTPFFNGYRPQFYFRTTDVTGTCDLPSGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV++ V L +P+A++ G +FAIREGGRTVGAGVV+ IIE
 Sbjct: 357 DNVQLVVS LHAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

tr Q5X873 Translation elongation factor Tu [tufA] [Legionella 396
 Q5X873_LEGPA pneumophila AA
 (strain Paris)] align

Score = 555 bits (1430), Expect = e-157
 Identities = 278/400 (69%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAKEKE R PHVN+GTIGHV HGKTTL+AAI+ +++ K K YD ID AP+E+ERG
 Sbjct: 1 MAKEKFERKKPHVNVGTIGHVDHGKTTLTAAITTIMAKKYGGTAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI+T+H+EYE+ +RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
 Sbjct: 61 ITISTAHVEYESASRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVVFNLKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVF+NK S+Y+FPGDD PIV GSAL+ALE
 Sbjct: 121 LLSRQVGVPPIVVFNMKADMVDDPELLELVEMEVRDLLSSYDFPGDDIPIVVGSALKALE 180

Query: 181 EAKAGNVGEWGEKVL-KLMAEVD SYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTGRIER 239
 G + G K + KL+ +DSYIP P R+ +K FL+P+EDVFSI+GRGT VVTGR+E
 Sbjct: 181 ----GEDSDIGVKAIEKLVETMSYIPEPVRNIDKPFLLPIEDVFSISGRGT VVTGRVES 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+VKVG+EVEIVGIR TQKTT TGVEMFRK L++G AGDNVGVLLRGTK++EVERG VL
 Sbjct: 237 GIVKVGEEVEIVGIRDTQKTTCTGVEMFRKLLDEGRAGDNVGVLLRGTKRDEVERGQVLA 296

Query: 300 KPGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359
 KPG+I PH KFE E+YVLSKEEGGRHTEFF YRPQFY RTTDVTG+ LP GVEMVMPG
 Sbjct: 297 KPGTIKPHTKFEAEVYVLSKEEGGRHTPFFNGYRPQFYFRTTDVTGTCDLPSGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV++ V L +P+A++ G +FAIREGGRTVGAGVV+ IIE
 Sbjct: 357 DNVQLVVS LHAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

tr Q57J27 Protein chain elongation factor EF-Tu (Duplicate of 409
 Q57J27_SALCH tufA) [tufB] AA
 [Salmonella cholerae-suis (Salmonella enterica)] align

Score = 555 bits (1430), Expect = e-157
 Identities = 271/398 (68%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 ++KEKE RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG

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Sbjct: 16  VSKEKFERTKPHVNVGTIGHVDHGKTTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARG 75

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQOTREHI 120
        ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQOTREHI
Sbjct: 76  ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQOTREHI 135

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LL RQVGVP+I+VFLNK                               S Y+FPGDDTPIV GSAL+ALE
Sbjct: 136  LLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRSALKALE 195

Query: 181  EAKAGNVGEWGEKVLKILMAEVD SYIPTPERDTEKTFIMPVEDVFSIAGRGT VVTGRIERG 240
        EW K+++L +DSYIP PER +K FL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 196  -----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGT VVTGRVERG 250

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        ++KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL K
Sbjct: 251  IIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAK 310

Query: 301  PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360
        PG+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTT DVTG+I LPEGVEMVMPGD
Sbjct: 311  PGTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYRTT DVTGTIELPEGVEMVMPGD 370

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
        N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
Sbjct: 371  NIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 408

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sp " POA1H5      Elongation factor Tu (EF-Tu) [tufA] [Salmonella      393
    EFTU_SALTY typhimurium]                                     AA
                                                                align

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Score = 555 bits (1429), Expect = e-157
Identities = 271/397 (68%), Positives = 319/397 (80%), Gaps = 5/397 (1%)

```

Query: 2   AKEKFNRNTPHVNIGTIGHVHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI 61
        +KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+          + +D IDNAP+EK RGI
Sbjct: 1   SKEKFERTKPHVNVGTIGHVDHGKTTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI 60

Query: 62  TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQOTREHIL 121
        TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQOTREHIL
Sbjct: 61  TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQOTREHIL 120

Query: 122  LSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALEE 181
        L RQVGVP+I+VFLNK                               S Y+FPGDDTPIV GSAL+ALE
Sbjct: 121  LGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRSALKALE- 179

Query: 182  AKAGNVGEWGEKVLKILMAEVD SYIPTPERDTEKTFIMPVEDVFSIAGRGT VVTGRIERG 241
        EW K+++L +DSYIP PER +K FL+P+EDVFSI+GRGT VVTGR+ERG+
Sbjct: 180  ---GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGT VVTGRVERGI 235

Query: 242  VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301
        +KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL KP
Sbjct: 236  IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKP 295

Query: 302  GSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGDN 361
        G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTT DVTG+I LPEGVEMVMPGDN

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Sbjct: 296 GTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398

+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++

Sbjct: 356 IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

sp POA1H6 Elongation factor Tu (EF-Tu) [tufA] [Salmonella typhi] 393 AA
EFTU_SALTI

align

Score = 555 bits (1429), Expect = e-157

Identities = 271/397 (68%), Positives = 319/397 (80%), Gaps = 5/397 (1%)

Query: 2 AKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERGI 61

+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RGI

Sbjct: 1 SKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI 60

Query: 62 TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHIL 121

TI TSH+SY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHIL

Sbjct: 61 TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHIL 120

Query: 122 LSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAIEFPDDTPIVAGSALRALEE 181

L RQVGVP+I+VFLNK S Y+FPDDTPIV GSAL+ALE

Sbjct: 121 LGRQVGVPYIIVFLNKCDDDEELLELVEMEVRELLSQYDFPDGDDTPIVRSALKALE- 179

Query: 182 AKAGNVGEWGEKVLKMAEVDYSIPTPERDTEKTFILMPVEDVFSIAGRGTVVGTGRIERG 241

EW K+++L +DSYIP PER +K FL+P+EDVFSI+GRGTVVGTGR+ERG+

Sbjct: 180 ----GDAWEAKIIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVGTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301

+VVG+VEVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL KP

Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGDN 361

G+I PH KEE E+Y+LSK+EGGRHTPFF YRPQFY RTTDDVTG+I LPEGVEMVMPGDN

Sbjct: 296 GTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398

+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++

Sbjct: 356 IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

sp O31298 Elongation factor Tu (EF-Tu) [tuf] [Buchnera aphidicola] 394
EFTU_BUCAP (subsp. AA

Schizaphis graminum)]

align

Score = 555 bits (1429), Expect = e-157

Identities = 272/398 (68%), Positives = 318/398 (79%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60

M+KEKF R PH+N+GTIGHV HGKTTL+AAI+ VLS K + +D IDNAP+EK RG

Sbjct: 1 MSKEKFQRVKPHINVGTIGHVDHGKTTLTAAITTVLSKKYGGSSARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

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      ITI TSH+FY+TE RHYAHVDCPGHADY+KNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61 ITINTSHVEYDTELRYAHVDCPGHADYIKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL RQVGVP+I+VFLNK + Y+FPGDDTPI+ GSAL+ALE
Sbjct: 121 LLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRDLLTQYDFPGDDTPIIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      +W K+L L +D+YIP P+R ++ FL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 181 -----GDADWESKILDLSKFLDITYIPEPKRAIDQPFLLPIEDVFSISGRGT VVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGT KKEEVERGMVLCK 300
      +VKVG+VEVEIVGI+ T KTT TGVEMFRK L++G AG+NVGVLLRGT++E+ERG VL K
Sbjct: 236 IVKVGEEVEIVGIKTTKTTCTGVEMFRKLLDEGRAGENVGVLLRGT KRDEIERGQVLAK 295

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360
      PGSI PH FE E+YVLSKEEGGRHTPFF YRPQFY RTT DVTGSI LPEGVEMVMPGD
Sbjct: 296 PGSIHPHTTFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTT DVTGSIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      N+K+TV LL P+A+ G +FAIREGGRTVGAGVVS ++
Sbjct: 356 NIKMTVTLIHPIAMADGLRFAIREGGRTVGAGVVS KVL 393

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tr Q6FZC0 Elongation factor tu (EF-tu) [tuf1] [Bartonella quintana] 391 AA
 Q6FZC0_BARQU (Rochalimaea quintana)]

align

Score = 555 bits (1429), Expect = e-157

Identities = 277/399 (69%), Positives = 322/399 (80%), Gaps = 8/399 (2%)

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Query: 1 MAKEKENRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK KE RT PHVNIGTIGHV HGKT+L+AAI+ K E K YD ID AP+E+ RG
Sbjct: 1 MAKSKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEERARG 55

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI+T+H+EYETE RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 56 ITISTAHVEYETEKRYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 115

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP IVVFLNK S Y+FPGDD PIV GSAL ALE
Sbjct: 116 LLARQVGVPPIVFLNKVDQVDDAEELLELEIRELLSKYDFPGDDIPIVKGSALE 175

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      + K ++GE + V LM+EVD+YIPTPER ++ FL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 176 D-KDKSIGE--DAVRLLMSEVDNYIPTPERPVDQPFLLPIEDVFSISGRGT VVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGT KKEEVERGMVLCK 300
      V+KVG+E+EI+GIR T KTTVTGVEMFRK L++G+AGDN+G LERG +E +ERG VL K
Sbjct: 233 VIKVGEEIEIIGIRPTSKTTVTGVEMFRKLLDQGGAGDNIGALLRGVDREGIERGQVLAK 292

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360
      PGS+TPH +F+ E Y+L+K+EGGRHTPFFTNYRPQFY RTT DVTG +TLPEG+EMVMPGD
Sbjct: 293 PGSVTPHTRFKAAYILTKDEGGRTHTPFFTNYRPQFYFRTT DVTGIVTLPEGIEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 399

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NV + V LL P+A+E +FAIREGGRTVGAG+VS IIE
 Sbjct: 353 NVAMDVSLIVPIAMEEKLRF AIREGGRTVGAGIVSKIIE 391

tr Q5WZL4 Elongation factor Tu [tufA] [Legionella pneumophila 396
 Q5WZL4_LEGPL (strain Lens)] AA
align

Score = 555 bits (1429), Expect = e-157
 Identities = 277/400 (69%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAKEKE R PHVN+GTIGHV HGKTTL+AAI+ +++ K K YD ID AP+E+ERG
 Sbjct: 1 MAKEKFERKKPHVNVGTIGHVDHGKTTLTAAITTIMAKKYGGTAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI+T+H+EYE+ +RHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI
 Sbjct: 61 ITISTAHVEYESASRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LLSRQVGVP+IVVF+NK S+Y+FPGDD FL+ GSAL+ALE
 Sbjct: 121 LLSRQVGVPYIVVFMNKADMVDDPELLELVEMEVRDLLSSYDFPGDDIPIVGSALKALE 180

Query: 181 EAKAGNVGEWGEKVL-KLMAEVD SYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIER 239
 G + G K + KL+ +DSYIP P R+ +K FL+P+EDVFSI+GRGT VVTGR+E
 Sbjct: 181 ----GEDSDIGVKAIEKL VETMSYIPEPVRNIDKPFLLPIEDVFSISGRGT VVTGRVES 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
 G+VKG+VEVEIVGIR TQKTT TGVEMFRK L++G AGENVGVLLRGTK++EVERG VL
 Sbjct: 237 GIVKVGEEVEIVGIRDTQKTTCTGVEMFRKLLDEGRAGDNVGVLLRGTKRDEVERGQVLA 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPOFYVRTTDVTGSITLPEGVEMVMPG 359
 KPG+I PH KFE E+YVLSKEEGGRHTPFF YRQFY RTTIVTG+ LP GVEMVMPG
 Sbjct: 297 KPGTIKPHTKFEAEVYVLSKEEGGRHTPFFNGYRPOFYFRTTDVTGTCDLPSGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 DNV++ V L +P+A++ G +FAIREGGRTVGAGV+ IIE
 Sbjct: 357 DNVQLVVS LHAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

sp Q925Y6 Elongation factor Tu (EF-Tu) [tufA] [Rhizobium meliloti 391 AA
 EFTU_RHIME (Sinorhizobium meliloti)]
align

Score = 554 bits (1428), Expect = e-156
 Identities = 276/399 (69%), Positives = 320/399 (80%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MAK KF R PHVNIGTIGHV HGKT+L+AAI+ K E K YD ID AP+EK RG
 Sbjct: 1 MAKSKFERNKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEEKARG 55

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
 ITI+T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI
 Sbjct: 56 ITISTAHVEYETPNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 115

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP IVVFLNK S+Y+EPGDD PIV GSAL ALE
 Sbjct: 116 LLARQVGVPPIVFLNKVDQVDDAEELLELEVEIRELLSSYEFPGDDIPIVKGSAALALE 175

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
 ++ +GE + + +LMA VD+YIPTPER ++ FIMP+EDVFSI+GRGT VVTGR+ERG
 Sbjct: 176 DSDK-KIGE--DAIRELMAAVDAYIPTPERPIDQPFLMPIEDVFSISGRGT VVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VKVG+E+EI+GIR T KTT TGVEMFRK L++G+AGDN+G LLRG + VERG +LCK
 Sbjct: 233 IVKVGEEIEIVGIRPTTKTTCTGVEMFRKLLDQGGAGDNIGALLRGVDRNGVERGQILCK 292

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360
 PGS+ PH+KF+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTENVG +TLPEG EMVMPGD
 Sbjct: 293 PGSVKPHRKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTT DVTGIVTLPEGTEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV + VELI P+A+E +FAIREGGRTVGAG+V++I+E
 Sbjct: 353 NVTVDVELIVPIAMEEKLRF AIREGGRTVGAGIVASIVE 391

tr Q6FZL2 Elongation factor tu (EF-tu) [tuf2] [Bartonella quintana 391 AA
 Q6FZL2_BARQU (Rochalimaea quintana)]

align

Score = 554 bits (1428), Expect = e-156

Identities = 277/399 (69%), Positives = 322/399 (80%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF RT PHVNIGTIGHV HGKT+L+AAI+ K E K YD ID AP+E+ RG
 Sbjct: 1 MAKSKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPERARG 55

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI+T+H+EYETE RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI
 Sbjct: 56 ITISTAHVEYETEKRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 115

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL+RQVGVP IVVFLNK S Y+EPGDD PIV GSAL ALE
 Sbjct: 116 LLARQVGVPPIVFLNKVDQVDDAEELLELEVEIRELLSKYDFPGDDIPIVKGSAALALE 175

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
 + K ++GE + V LM+EV D+YIPTPER ++ FL+P+EDVFSI+GRGT VVTGR+ERG
 Sbjct: 176 D-KDKSIGE--DAVRLLMSEVDNYIPTPERPIDQPFLPIEDVFSISGRGT VVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 V+KVG+E+EI+GIR T KTTVTGVEMFRK L++G+AGDN+G LLRG +E +ERG VL K
 Sbjct: 233 VIKVGEEIEIIGIRPTSKTTVTGVEMFRKLLDQGGAGDNIGALLRGVDREGIERGQVLAK 292

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360
 PGS+TPH +F+ E Y+L+K+EGGRHTPFFTNYRPQFY RTTENVG +TLPEG+EMVMPGD
 Sbjct: 293 PGSVTPHTRFKAEAYILTKDEGGRTHTPFFTNYRPQFYFRTT DVTGIVTLPEGIEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV + V LI P+A+E +FAIREGGRTVGAG+VS IIE
 Sbjct: 353 NVAMDVSLIVPIAMEEKLRF AIREGGRTVGAGIVSKIIE 391

tr Q7MYE8 **Elongation factor Tu (EF-Tu) [tufA] [Photorhabdus** 394
 Q7MYE8_PHOLL **luminescens** AA
 (subsp. laumondii)] align

Score = 554 bits (1428), Expect = e-156
 Identities = 269/398 (67%), Positives = 321/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 M+KEKE RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D LEMAP+EK RG
 Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGNARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI+TSH+EY+T +RHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGMPQTREHI
 Sbjct: 61 ITISTSHVEYDTPSRHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP+I+VFLNK S Y+FEQDDTP++ GSAL+ALE
 Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELEVMEVRELLSQYDFPGDDTPVIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVVGRIERG 240
 EW K+++L +DSYIP PER ++ FL+P+EDVFSI+GRGTVVVGRI+ERG
 Sbjct: 181 -----GDAEWEAKIIEALAEALDSYIPEPERAIDQPFLLPIEDVFSISGRGTVVVGRIERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VVKVG+EVEIVGI+ T KTT TGVMFRK L++G AG+NVGVLLRGTK++E+ERG VL K
 Sbjct: 236 IVKVGEEVEIVGIKDTTKTTCTGVMFRKLLDEGRAGENVGVLLRGTKRDEIERGQVIAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
 PGSI PH FE E+Y+LSK+EGGRHTPEE YRPQFY RTTDTVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGSIKPHTTFESEVYILSKDEGGRTTFFKGYRPFQFYFRTTDTVTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
 N+++ V LI+P+A++ G +FAIREGGRTVGAGVV+ +I
 Sbjct: 356 NIQMKVTLIAPIAMDQGLRFAIREGGRTVGAGVVAKVI 393

sp P18668 **Elongation factor Tu (EF-Tu) [tuf] [Synechococcus sp.** 409
 EFTU_SYN6 **(strain PCC** AA
 6301) (Anacystis nidulans)] align

Score = 554 bits (1427), Expect = e-156
 Identities = 278/409 (67%), Positives = 328/409 (79%), Gaps = 10/409 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 MA+ KE RT PH NIGTIGHV HGKTTL+AAI+ VL+ G+A+ + Y +ID AP+EK RG
 Sbjct: 1 MARAKFERTKPHANIGTIGHVDHGKTTLTAAITTVLAKAGMAKARAYADIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI
 Sbjct: 61 ITINTAHVEYETGNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
 LL++QVGVP+IVVFLNK S+Y+FEQDD PIVAGSAL+ALE
 Sbjct: 121 LLAQVGVPPIVFLNKEDMVDDAEELLELEVRELLSSYDFPGDDPIVAGSALQALE 180

Query: 181 EAKAGNVGE-----WGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTG 235
 + G G+ W +K+LKIM EVD+YIPTER+ ++ FLM VEDVF+I GRGTV TG
 Sbjct: 181 AIQGGASGQKGDNPWVDKILKLMEEVDAYIPTPEREVD RPFLMAVEDVFTITGRGT VATG 240

Query: 236 RIERGVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERG 295
 RIERG VKVG+ +EIVG+R T+ TTVTGVEMF+K L++G AGDNVG+LRG +K ++ERG
 Sbjct: 241 RIERGSVKVGETIEIVGLRDTRSTTVTGVEMFQKTLDEGLAGDNVGLLLRGIQKTDIERG 300

Query: 296 MVLCKPGSITPHKKFEE EIIYVLSKEEGGRHTPF FTYNRPQFYVRTTDVTGSI---TLPEG 352
 MVL KPGSITPH KFE E+YVL KEEGGRHTFFF YRPQFYVRTTDVTG+I T +G
 Sbjct: 301 MVLAKPGSITPHTKFES EYVVLKKEEGGRHTPFFPGYRPQFYVRTTDVTGAISDFTADDG 360

Query: 353 --VEMVMPGDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 EMV+PGD +K+TVELI+P+A+E G +FAIREGGRT+GAGVVS I++
 Sbjct: 361 SAAEMVIPGDRIKMTVELINPIAIEQGMRF AIREGGRTIGAGVVS KILQ 409

sp O31297 Elongation factor Tu (EF-Tu) [tuf] [Buchnera aphidicola] 394
 EFTU_BUCAI (subsp. AA
 Acyrthosiphon pisum) (Acyrtosiphon pisum symbiotic align
 bacterium)]

Score = 554 bits (1427), Expect = e-156
 Identities = 270/398 (67%), Positives = 319/398 (79%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 M+KEKF R PH+N+GTHGV NGKTTL+AAI+ VLS K + +D IDNAP+EK RG
 Sbjct: 1 MSKEKFQRLKPHINVGTIGHVDHGKTTLTAAITTVLSKKFGGSARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI TSH+RY+TE RHYAHVDCPGHADY+KNMITGAAQMDGAILVV+A DGMPQTREHI
 Sbjct: 61 ITINTSHVEYDTEFRHYAHVDCPGHADYIKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVP H I VFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
 LL RQVGVP+I+VFINK + Y+FPGDDTPI+ GSAL+ALE
 Sbjct: 121 LLGRQVGVPYII VFLNKCDMVDDEELLELVEMEVRDLLTQYDFPGDDTPIIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
 EW K++ L +DSYIP E+R ++ FL+P+EDVFSI+GRGT VVTGR+E+G
 Sbjct: 181 GDP-----EWESKIIDL SKFLDSYIPEPKRAVDQPFLLPIEDVFSISGRGT VVTGRVEKG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 ++KVG+EVEIVGI+ T NTT TGVEMFRK L++G AG+NVGVLLRGTK++E+ERG VL K
 Sbjct: 236 IIKVGEEVEIVGIKTTKTTCTGVEMFRKLLDEGRAGENVGVLLRGTKRDEIERGQVLAK 295

Query: 301 PGSITPHKKFEE EIIYVLSKEEGGRHTPF FTYNRPQFYVRTTDVTGSI TLPEGVEMVMPGD 360
 PCSI PH FE E+YVLSKEEGGRHTFFF YRPQFY RTTDVTGSI LPEG+EMVMPGD
 Sbjct: 296 PGSIHPHTTFESEYVLSKEEGGRHTPFFKGYRPQFYFR TTDVTGSIELPEGIEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 398
 N+K+TV LI+P+A+ G +FAIREGGRTVGAGVVS ++
 Sbjct: 356 NIKMTVTLINPIAMADGLRFAIREGGRTVGAGVVS KVL 393

sp P33165 Elongation factor Tu (EF-Tu) [tuf] [Bacteroides fragilis] 394 AA

EFTU_BACFR

align

Score = 553 bits (1426), Expect = e-156

Identities = 271/399 (67%), Positives = 317/399 (78%), Gaps = 5/399 (1%)

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Query: 1  MAKEKFNRNTPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MAKEKF RT PHVNIGTIGHV HCKTTL+AAI+ VL+ KGL+E++ +D+IDNAP+EKERG
Sbjct: 1  MAKEKFERTKPHVNIGTIGHVDHGKTTLTAAITTVLAKKGLSELRSFDSIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120
        ITI TSH+EYET RHYAHVDCPGHADVKNM+TGAAQMDGAI+VV+A DGMPQOTREHI
Sbjct: 61  ITINTSHVEYETANRHYAHVDCPGHADVKNMVTGAAQMDGAIIVVAATDGMPQOTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LL+RQV VP +VVF+NK S Y+F GD+TPI+ GSAL AL
Sbjct: 121  LLARQVNVPKLVVFMNKCMDVEDAEMLLEVEMRELLSFYDFDGDNTPIIQGSALGALN 180

Query: 181  EAKAGNVGEWGEKVLKMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVVGRIERG 240
        V +W +KV++LM VD++IP P RD +K FLMPVEDVEST GRGTV TGRLE G
Sbjct: 181  -----GVEKWEDKVMELMEAVDTWIPLPRDVKPFLMPVEDVFSITGRGTVATGRIETG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300
        V+ VGDE+ET+G+ +K+ VTGVEMFRK L++GEAGDNVG+LLRG K E++RGMVLCK
Sbjct: 236  VIHVGDEIEILGLGEDKKS SVTVGVEMFRKLLDQGEAGDNVGLLLRGVDKNEIKRGMVLCK 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSITLPEGVEMVMPGD 360
        PG I PH KF+ E+Y+L KEEGGRHTPE YRPQFY+RT D TG ITLPEG EMVMPGD
Sbjct: 296  PGQIKPHSKFKAENVYILKKEEGGRHTPFHNKYRPQFYLRMTDCTGEITLPEGTEMVMPGD 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
        NV ITVELI EVAL +G +FAIREGGRTVGAG ++ II+
Sbjct: 356  NVTITVELIYPVALNIGLRFAIREGGRTVGAGQITEIID 394

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sp P33171      Elongation factor Tu (EF-Tu) [tuf] [Synechococcus sp.      409
   EFTU_SYNP7 (strain PCC
               7942) (Anacystis nidulans R2)]
                                     AA
                                     align

```

Score = 553 bits (1424), Expect = e-156

Identities = 277/409 (67%), Positives = 328/409 (79%), Gaps = 10/409 (2%)

```

Query: 1  MAKEKFNRNTPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MA+ KF RT PH NIGTIGHV HCKTTL+AAI+ VL+ G+A+ + Y +ID AP+EK RG
Sbjct: 1  MARAKFERTKPHANIGTIGHVDHGKTTLTAAITTVLAKAGMAKARAYADIDAAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120
        ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI
Sbjct: 61  ITINTAHVEYETGNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LL++QVGVP+IVVFLNK S+Y+FPGDD PIVAGSAL+ALE
Sbjct: 121  LLAKQVGVPNIVVFLNKEDMVDDAELLELEVELEVRELLSSYDFPGDDIPIVAGSALQALE 180

Query: 181  EAKAGNVGE-----WGEKVLKMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVVG 235
        + G G+ W +K+LKLM EVD+YIPTER+ ++ FLM VEDVF+I GRGTV TG
Sbjct: 181  AIQGGASGQKGNPWVDKILKLMEEVDAYIPTPEREVDPRPFLMAVEDVFTITGRGTVATG 240

```

Query: 236 RIERGVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERG 295
 RIERG VKVG+ +EIVG+R T+ TTVTGVEMF+K L++G AGDNVG+ILRG +K ++ERG
 Sbjct: 241 RIERGSVKVGETIEIVGLRDRSTTTVTGVEMFQKTLDEGLAGDNVGLLLRGIQKTDIERG 300

Query: 296 MVLCKPGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPOFYVRTTDDVTGSI---TLPEG 352
 MVL KPGSITPH KFE E+YVL K+EGGRHTPEE YRPQFYVRTTDDVTG+I T +G
 Sbjct: 301 MVLAKPGSITPHTKFESEVYVLKKDEGGRHTPFFPGYRPOFYVRTTDDVTGAISDFTADDG 360

Query: 353 --VEMVMPGDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 EMV+PGD +K+TVELL+P+A+E G +FAIREGGRT+GAGVVS I++
 Sbjct: 361 SAAEMVIPGDRIKMTVELINPIAIEQGMRFIREGGRTIGAGVVSILQ 409

sp Q8ZAN8 Elongation factor Tu-B (EF-Tu-B) [tufB] [Yersinia pestis] 394 AA
 EFTU2_YERPE

align

Score = 553 bits (1424), Expect = e-156
 Identities = 271/399 (67%), Positives = 319/399 (79%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
 M+KEKE RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IINAP+EK RG
 Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGSARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120
 ITI TSH+EX+T RHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGPMPQTREHI
 Sbjct: 61 ITINTSHVEYDTPARHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDPTPIVAGSALRALE 180
 LL RQVGVP+I+VELNK S Y+FPGDPT++ GSAL+ALE
 Sbjct: 121 LLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDPTPIVIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
 EW K+++L +DSYIP PER ++ FL+P+EDVFSI+GRGTVVTGR+ERG
 Sbjct: 181 -----GDAEWEAKIIEALAEALDSYIPQPERAIDRPFLLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
 +VVKVG+EVEIVGI T KTT TGVEMFRK L++G AG+NVGVLLRGTK+++V+RG VL K
 Sbjct: 236 IVKVGEEVEIVGIIDTIKTCTGVEMFRKLLDEGRAGENVGVLLRGTKRDDVQRGQVLAK 295

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPOFYVRTTDDVTGSIITLPEGVEMVMPGD 360
 PGSI PH KFE E+Y+LSK+EGGRHTPEE YRPQFY RTTDDVTG+I LPEGVEMVMPGD
 Sbjct: 296 PGSIKPHTKFESEVYILSKDEGGRHTPFFKGYRPOFYFRTTDDVTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV + V LI+P+A++ G +FAIREGGRTVGAGVV+ +IE
 Sbjct: 356 NVNMVNLIAPIAMDDGLRFAIREGGRTVGAGVVAKVIE 394

tr Q66FQ9 Elongation factor Tu [tufA] [Yersinia
 Q66FQ9_YERPS pseudotuberculosis]

394
 AA
align

Score = 553 bits (1424), Expect = e-156

Identities = 271/399 (67%), Positives = 319/399 (79%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
        M+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+      + +D IDNAP+EK RG
Sbjct: 1  MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGSARAFDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI TSH+EY+T RHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI
Sbjct: 61  ITINTSHVEYDTPARHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LL RQVGVP+I+VELNK                               S Y+FPGDDT++ GSAL+ALE
Sbjct: 121  LLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPVIRGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
        EW K+++L +DSYIP PER ++ FL+P+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181  -----GDAEWEAKIIELAEALDSYIPQPERAIDRPFLPIEDVFSISGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        +VVKVG+EVEIVGI T KTT TGVEMFRK L++G AG+NVGVLLRGTK+++V+RG VL K
Sbjct: 236  IVKVGEEVEIVGIIDTIKTTCTGVEMFRKLLDEGRAGENGVLLRGTKRDDVQRGQVLAK 295

Query: 301  PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
        PGSI PH KFE E+Y+LSK+EGGRHTFFF YRPQFY RTTDTVGS+I LPEGVEMVMPGD
Sbjct: 296  PGSIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDTVGTIELPEGVEMVMPGD 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
        NV + V LI+P+A++ G +FAIREGGRTVGAGV+ +IE
Sbjct: 356  NVNMVNLIAPIAMDDGLRFAIREGGRTVGAGVAKVIE 394

```

tr Q8KHX9 **Elongation factor TU (EF-Tu) [tufB] [Bartonella henselae 391 AA**
Q8KHX9_BARHE **(Rochalimaea henselae)]**

[align](#)

Score = 552 bits (1423), Expect = e-156

Identities = 278/399 (69%), Positives = 320/399 (79%), Gaps = 8/399 (2%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
        MAK KF RT PHVNIGTIGHV HGKT+L+AAI+      K   E K YD ID AP+E+ RG
Sbjct: 1  MAKSKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEERARG 55

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI+T+H+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI
Sbjct: 56  ITISTAHVEYETEKRYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 115

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LL+RQVGVP IVVFLNK                               S Y+FPGDD PIV GSAL ALE
Sbjct: 116  LLARQVGVPPIVFLNKVDQVDDAEELLELEVRELLSKYDFPGDDIPVKGSALE 175

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
        + K   ++GE + V LM+EVD+YIPTPER ++ FLMP+EDVFSI+GRGTVVTGR+ERG
Sbjct: 176  D-KDKSIGE--DAVRLLMSEVDNYIPTPERPVDQPFMLPIEDVFSISGRGTVVTGRVERG 232

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        V+KVG+EVEI+GIR T KTTVTGVEMFRK L++G+AGDN+G LLRG +E +ERG VL K

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Sbjct: 233 VIKVGEEVEIIGIRPTSKTTVTGVMFRKLLDQGQAGDNIGALLRGIDREGIERGQVLAK 292

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
 P S+TPH +P+ E Y+L+K+EGGRHTPFFTNYRPQFY RTTDTG +TLPEG EMVMPGD

Sbjct: 293 PASVTPHTRFKAEAYILTKDEGGRHTPFFTNYRPQFYFRTTDTVGIVTLPEGTEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 NV + V LI P+A+E +FAIREGGRTVGAG+VS IIE

Sbjct: 353 NVAMDVSLIVPIAMEEKLRFIREGGRTVGAGIVSKIIE 391

tr Q89J82 Elongation factor TU [tuf] [Bradyrhizobium japonicum] 396 AA
Q89J82_BRAJA

align

Score = 552 bits (1423), Expect = e-156
 Identities = 276/401 (68%), Positives = 321/401 (79%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
 MAK KF R PH NIGTIGHV HGKT+L+AAI+ +L+ G A YD ID AP+EK RG

Sbjct: 1 MAKAKFERNKPHCNIGTIGHVDHGKTSLTAAITKILAETGGATFTAYDQIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
 ITI+T+H+EYET+ RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI

Sbjct: 61 ITISTAHVEYETKNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVP HIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGD DTPIVAGSALRALE 180
 LL+RQVGVP +VVFLNK S YEFPGD PI+ GSAL ALE

Sbjct: 121 LLARQVGVPALVVFLNKCDMVDDPELLELVELEVRELLSKYEFPGD KPIIKGSALAALE 180

Query: 181 EA--KAGNVGEWGEKVLKLMAEVD SYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIE 238
 ++ K G+ + +L+LM VD YIP PER ++ ELMFVEDVESI+GRGT VVTGR+E

Sbjct: 181 DSDKKLGH-----DAILELMRNVDEYIPQPERPIDQPF LMPVEDVFSISGRGT VVTGRVE 235

Query: 239 RGVVKGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298
 RG+VVG+E+EIVG+RATQKTTVTGVMFRK L++G+AGDN+G LLRGTK+E+VERG VL

Sbjct: 236 RGIVKVGEEIEIVGLRATQKTTVTGVMFRKLLDQGQAGDNIGALLRGTKREDVERGQVL 295

Query: 299 CKPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMP 358
 KPGS+ PH KT+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTDTG + LPEG EMVMP

Sbjct: 296 AKPGSVKPHTKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTTDTGVVHLPEGTEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
 GDN+ + V LI P+A+E +FAIREGGRTVGAGV++IIE

Sbjct: 356 GDNIAEVHLIVPIAMEEKLRFIREGGRTVGAGVVASIIE 396

tr Q727D5 Translation elongation factor Tu [tuf] [Desulfovibrio] 397
Q727D5_DESVH vulgaris AA
 (strain Hildenborough / ATCC 29579 / NCIMB 8303)] align

Score = 552 bits (1423), Expect = e-156
 Identities = 271/399 (67%), Positives = 319/399 (79%), Gaps = 2/399 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60

```

      M KEKF R PHVNIGTIGH+ HGKTTL+AAI+ L G + YD ID AP+EKERK
Sbjct: 1 MGKEKFERKKPHVNIGTIGHIDHGKTTLTAAITKTAGLLQGKFIAFYDEIDKAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITIAT+H+EYET TRHYAHVDCPGHADV+KNMITGAAQMDGAI+VV+A DGPMPQTREHI
Sbjct: 61 ITIATAHVEYETATRHYAHVDCPGHADYIKNMITGAAQMDGAIIVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+IVVFLNK + + Y FEGDD P+V GSAL+ALE
Sbjct: 121 LLARQVGVPYIIVVFLNKCDMVDDEELLELEVELEVRELLTSYGFPGDDVPVVRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
      + + + + L+A DSYIF P+RD +K FLMP+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181 SDDPNS--DACKPIRELLAACDSYIPEPQRDIDKPFMLPIEDVFSISGRGTVVTGRVERG 238

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      V+KVG+EVEIVGI+ T K+T TGVEMFRK L++G+AGDN+G LLRG K+++VERG VL
Sbjct: 239 VIKVGEEVEIVGIKDTTKSTCTGVEMFRKLLDQGGAGDNIGALLRGVVKRDDVERGQVLAA 298

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
      P SITPH+KF+ E+YVLSKEEGGRHTPFET+ YRPQFY RTTD+TG ITL EGVEMVMPGD
Sbjct: 299 PKSITPHRKFAEVYVLSKEEGGRHTPFSSGYRPQFYFRTTDTITGVITLEEGVEMVMPGD 358

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      N VELI+P+A+ELG +FAIREGGRTVGAGVVS I+E
Sbjct: 359 NATFNVELIAPIAMELGRLFAIREGGRTVGAGVVSEIVE 397

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tr Q7N9B1 Translation elongation factor EF-Tu.B [tufB] 394
Q7N9B1_PHOL [Photorhabdus luminescens (subsp. laumondii)] AA
align

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Score = 552 bits (1422), Expect = e-156
 Identities = 268/398 (67%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

```

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      M+KEKF R PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IENAP+EK RG
Sbjct: 1 MSKEKFERKKPHVNVGTIGHVDHGKTTLTAAITTVLAKTFGGNARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI+TSH+EY+T +RHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGPMPQTREHI
Sbjct: 61 ITISTSHVEYDTPSRHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LL RQVGVP+I+VFLNK S Y+FPGDDTF++ GSAL+ALE
Sbjct: 121 LLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRLLSQYDFPGDDTPVIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
      EW K++L +DSYIP PER ++ FL+P+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181 -----GDAEWEAKIIEIAEALDSYIPEPERAIDQPFLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +VVKVG+EVEIVGI+ T KTF TGVEMFRK L++G AG+NVGVLLRGTK++E+ERG VL K
Sbjct: 236 IVKVGEEVEIVGIKDTTKTTCTGVEMFRKLLDEGRAGENGVLLRGTKRDEIERGQVLAK 295

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360

```

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PGSI PR FE E+Y+LSK+EGGRATPEE YRPQFY RTTDVGTG+I LPEGVEMVMPGD
Sbjct: 296 PGSIKPHTTFESEVYILSKDEGGRHTPFFFKGYRPPQFYFRTTDVGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      N+++ V LI+P+A++ G +FAIREGGRTVGAGVV+ +I
Sbjct: 356 NIQMKVTLIAPIAMDQGLRFAIREGGRTVGAGVVAKVI 393

```

```

sp Q8UE16      Elongation factor Tu (EF-Tu) [tufA] [Agrobacterium      391
  EFTU_AGRT5  tumefaciens
               (strain C58 / ATCC 33970)]
               align

```

Score = 551 bits (1421), Expect = e-156
 Identities = 274/399 (68%), Positives = 320/399 (79%), Gaps = 8/399 (2%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK KF R PHVNIGTIGHV HGKT+L+AAI+ K E K YD ID AP+EK RG
Sbjct: 1  MAKSKFERNKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEEKARG 55

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI+T+H+EYET RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 56  ITISTAHVEYETPARHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 115

Query: 121  LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP IVVFLNK S+Y+FPGDD PI+ GSAL ALE
Sbjct: 116  LLARQVGVPPIVVFLNKVDQVDDAELELLEVELEVRELLSSYDFPGDDIPIIKGSALAALE 175

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVVTGRIERG 240
      ++ +GE + + +LMA VD+YIPTER ++ FILMP+EDVFSI+GRGTVVVTGR+ERG
Sbjct: 176  DSDK-KIGE--DAIRELMAAVDAYIPTPERPIDQPFLMPIEDVFSISGRGTVVVTGRVERG 232

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVMERFKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +VKVG+EVEIVGIR T KTTVTGVMERK L+*G+AGDN+G L+RG ++ VERG +LCK
Sbjct: 233  IVKVGEEVEIVGIRPTS KTTVTGVMERKLLDQGGAGDNIGALVRGVTRDGVVERGQILCK 292

Query: 301  PGSITPHKKFEEIEIYVLSKEEGGRHTPFFFTNYRPPQFYVRTTDVTSITLPEGVEMVMPGD 360
      PGS+ PHKKF E Y+L+KEEGGRHTPFFFTNYRPPQFY RTTDVGTG ++LPEG EMVMPGD
Sbjct: 293  PGSVKPHKKFMAEAYILTKEEGGRHTPFFFTNYRPPQFYFRTTDVGTGIVSLPEGTEMVMPGD 352

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 399
      NV + VELL P+A+E +FAIREGGRTVGAG+V++I+E
Sbjct: 353  NVTVEVELIVPIAMEEKLRF AIREGGRTVGAGIVASIVE 391

```

Database: EXPASY/UniProtKB

Posted date: Jun 6, 2005 10:37 AM

Number of letters in database: 640,866,274

Number of sequences in database: 1,974,938

Lambda	K	H
0.315	0.135	0.383

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
length of query: 399
length of database: 640,866,274
effective HSP length: 128
effective length of query: 271
effective length of database: 388,074,210
effective search space: 105168110910
effective search space used: 105168110910
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (22.0 bits)
S2: 75 (33.5 bits)

Wallclock time: 18 seconds

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